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- GRAY SCALE DOCUMENTS

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AΒ

L6	ILE 'REGISTRY' ENTERED AT 14:27:22 ON 07 OCT 2003 1217 S ATPASE?/CN - Key term	nS.				
FILE 'HCAPLUS' ENTERED AT 14:27:30 ON 07 OCT 2003  L6 1217 SEA FILE=REGISTRY ABB=ON PLU=ON ATPASE?/CN  L7 166 SEA FILE=HCAPLUS ABB=ON PLU=ON (PLASMODIUM OR FALCIPARU  M) AND (L6 OR ATPASE OR ADENOSINE(2W) (TRIPHOSPHATASE OR  TRI PHOSPHATASE))						
L8	L8 4 SEA FILE=HCAPLUS ABB=ON PLU=ON L7 AND (MICROTUB? OR MICRO TUBUL?)					
L6 L7						
L9	L9 87 SEA FILE=HCAPLUS ABB=ON PLU=ON L7 AND (PROTEIN OR PEPTIDE OR POLYPROTEIN OR POLYPEPTIDE)					
L1 <u>0</u>						
L12 11 L8 OR L10						
L12 ANSWER 1 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN						
ACCESSION NUMBER: 2003:454501 HCAPLUS DOCUMENT NUMBER: 139:35072						
TITLE: Vectors comprising nucleotide sequences for						
	HERNA mRNA, and their uses including use as					
vaccines INVENTOR(S): McCreavy, David Thomas; Fraser, William Duncan; Gallagher, James Anthony						
PATENT ASSIGNEE(S): University of Liverpool, UK						
SOURCE: PCT Int. Appl., 52 pp. CODEN: PIXXD2						
DOCUMENT TYPE: Patent LANGUAGE: English						
FAMILY ACC. NUM. COUNT: 1 PATENT INFORMATION:						
	ATENT NO. KIND DATE APPLICATION NO. DATE					
WO 2003048371 A2 20030612 WO 2002-GB5512 20021206						
	O 2003048371 A3 20030912					
	CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,					
	GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,					
	NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ,					
	TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM,					
	AZ, BY, KG, KZ, MD, RU, TJ, TM  PW. CH CM KE IS MW MZ SD SI SZ TZ UC ZM ZW AT BE					
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU,					
	MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN,					
חחדר	GQ, GW, ML, MR, NE, SN, TD, TG					
PRIORITY APPLN. INFO.: GB 2001-29338 A 20011207 GB 2002-23829 A 20021012						

Searcher: Shears 308-4994

RITY APPLN. INFO.:

GB 2001-29338 A 20011207

GB 2002-23829 A 20021012

The invention provides vectors (such as viral vectors, plasmid

vectors or phagemids) comprising: (a) a heterologous nucleotide sequence encoding an antigenic polypeptide from a pathogen (such as viral, bacterial, parasitic or fungal); (b) a nucleotide sequence encoding a protease inhibitor (such as human PI31); a nucleotide sequence for a constitutive, regulatable, and/or cell/tissue-specific promoter; and (d) a nucleotide sequence encoding an inhibitory RNA mols., specifically an antisense human HERNA oligonucleotides. The invention also provides vectors comprising a nucleotide sequence encoding CIITA, a polypeptide that stimulates the expression of MHC The invention further provides the use of said class II genes. vectors as vaccines in production of an immune response (humoral) to said antigens in an animal, such as human, wherein said vaccination may be against a viral, fungal, bacterial or parasitic disorder. Still further, the invention relates: (a) using said vectors in production of antibodies, wherein said antibodies may be of therapeutic and/or of diagnostic use; (b) that said vectors may be adapted for expression of humanized or chimeric antibodies; and (c) that said vectors may be used to used to immunize animals for production of hybridomas expressing a monoclonal antibody against antigen of interest. Finally, the invention provides the cDNA sequences of mouse CIITA, and human PI31, and partial cDNA sequence of human HERNA helicase. The invention related that the use of said vectors containing said sequences can be used to enhance secretion of translated immunogen, and enhance DNA vaccination bias away from an MHC class I event towards MHC class II event. In the examples, the invention presented the construction of two vectors, pcDNAFinal and pcDNA6TR-IRES-CIITA, wherein pcDNAFinal contains nucleotide sequences encoding immunogen parathyroid hormone-related protein (PTHrP), antisense HERNA mRNA, PI31 and CD4+ T-cell epitope from lymphocytic choriomeningitis virus and wherein pcDNA6TR-IRES-CIITA encodes CIITA. Specifically, the invention related that: (a) antisense HERNA RNA can increase the transcriptional efficiency of vectors resulting in greater levels of transgene expression; (b) PI31 can inhibit proteasome digestion of recombinant antigen making it more assessable to MHC class II antigens; (c) inclusion of CD4+ T-cell epitope ensured that degraded immunogen-MHC class II complex bound to CD4+ T cells; and (d) inclusion of CIITA protein allowed for over-expression of MHC class II antigens.

IT 9000-83-3, Atpase

RL: BSU (Biological study, unclassified); BIOL (Biological study) (promoter of; vectors comprising sequences for promoter, target immunogen, PI31, CIITA and antisense HERNA mRNA, and their uses, including as vaccines towards various disorders)

L12 ANSWER 2 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2003:454460 HCAPLUS

DOCUMENT NUMBER: 139:31820

TITLE: Plasmodium falciparum

kinesin motor protein KinI-1 with

microtubule-stimulated

ATPase activity and uses for diagnosis

and treatment of malaria

Sakowicz, Roman; Beraud, Christophe; Guo, Jun; INVENTOR(S):

Freedman, Richard

PATENT ASSIGNEE(S): Cytokinetics, Inc., USA PCT Int. Appl., 68 pp.

SOURCE:

CODEN: PIXXD2

DOCUMENT TYPE: LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT INFORMATION:						
PATENT NO. K		APPLICATION NO.	DATE			
WO 2003048320	A2 20030612	WO 2002-US38360	20021127			
		BA, BB, BG, BR, BY				
CN, CO, CR	, CU, CZ, DE, DK,	DM, DZ, EC, EE, ES	, FI, GB, GD,			
GE, GH, GM	, HR, HU, ID, IL,	IN, IS, JP, KE, KG	, KP, KR, KZ,			
		MA, MD, MG, MK, MN				
		RU, SC, SD, SE, SG				
		UG, US, UZ, VC, VN	, YU, ZA, ZM,			
	, BY, KG, KZ, MD,		713 AM DE			
		SL, SZ, TZ, UG, ZM ES, FI, FR, GB, GF				
		BJ, CF, CG, CI, CM				
GW. MI. MR	, NE, SN, TD, TG	Bo, cr, cd, cr, cr	i, on, on, og,			
US 2003104496	A1 20030605	US 2001-6780	20011130			
PRIORITY APPLN. INFO.:		US 2001-6780 A2				
		US 2002-86935 A2	20020228			
AB The present invent	ion relates to <b>pr</b>	otein and cDNA				
sequences of a new						
		the use of these com				
		evention of malaria				
	invention provides isolated nucleic acid and amino acid sequences of kinesin superfamily motor <b>protein</b> KinI-1, which has					
microtubule stimul		The invention furt	her			
relates to antibod	ies to PfKinT-1.	methods of screening	ng for PfKinT-1			
		I-1, and kits for s				
PfKinI-1 modulator		,	<b>.</b>			
IT 9000-83-3, ATPase						
	RL: BSU (Biological study, unclassified); BIOL (Biological study)					
(microtubule-st	(microtubule-stimulated; Plasmodium					
	falciparum kinesin motor protein KinI-1 with					
microtubule-sti						
activity and us	es for diagnosis	and treatment of ma	laria)			
L12 ANSWER 3 OF 11 HC	APLUS COPYRIGHT	2003 ACS ON STN				
ACCESSION NUMBER:	2003:435206 HC					
DOCUMENT NUMBER:	139:909	AL 100				
TITLE:	(Sequences of P)	asmodium	a li,			
		esin KinI-1 and use	for >			
	freating malari		1,57.0			
INVENTOR(S):	Sakowicz, Romar	; Beraud, Christoph	ie; Guo, Jun;			
14.	Freedman, Richa					
PATENT ASSIGNEE(S):	Cytokinetics, 1					
SOURCE:	U.S. Pat. Appl.	Publ., 32 pp.				
	CODEN: USXXCO					
DOCUMENT TYPE:	Patent					
LANGUAGE:	English					
FAMILY ACC. NUM. COUNT:	2					
PATENT INFORMATION:						

PATENT NO. KIND DATE APPLICATION NO. DATE

US 2001-6780

20011130

US 2003104496

Α1

20030605

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WO 2002-US38360 20021127
                            A2
      WO 2003048320
                                   20030612
               AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
                ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
           RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
                GW, ML, MR, NE, SN, TD, TG
                                                  US 2001-6780
PRIORITY APPLN. INFO.:
                                                                       A2 20011130
                                                  US 2002-86935
                                                                       A2 20020228
      The invention provides sequences of Plasmodium
AB
      falciparum kinesin KinI-1. The invention also relates to
      the use of KinI-1 for the diagnosis, treatment, or prevention of
      malaria.
IT
      9000-83-3, ATPase
      RL: BSU (Biological study, unclassified); BIOL (Biological study)
          (microtubule-stimulated; sequences of
          Plasmodium falciparum kinesin KinI-1 and use
          for treating malaria)
L12 ANSWER 4 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                               2002:752115 HCAPLUS
DOCUMENT NUMBER:
                               137:289734
TITLE:
                               Sequence of Plasmodium
                               falciparum chromosomes 2, 10, 11 and 14
                               Gardner, Malcolm J.; Shallom, Shamira J.;
AUTHOR(S):
                               Carlton, Jane M.; Salzberg, Steven L.; Nene,
                               Vishvanath; Shoaibi, Azadeh; Ciecko, Anne; Lynn,
                               Jeffery; Rizzo, Michael; Weaver, Bruce; Jarrahi,
                               Behnam; Brenner, Michael; Parvizi, Babak;
                               Tallon, Luke; Moazzez, Azita; Granger, David;
                               Fujii, Claire; Hansen, Cheryl; Pederson, James;
                               Feldblyum, Tamara; Peterson, Jeremy; Suh,
Bernard; Angiuoli, Sam; Pertea, Mihaela; Allen,
                               Jonathan; Selengut, Jeremy; White, Owen;
                               Cummings, Leda M.; Smith, Hamilton O.; Adams,
                               Mark D.; Venter, J. Craig; Carucci, Daniel J.;
                               Hoffman, Stephen L.; Fraser, Claire M.
CORPORATE SOURCE:
                               The Institute for Genomic Research, Rockville,
                               MD, 20850, USA
SOURCE:
                               Nature (London, United Kingdom) (2002),
                               419(6906), 531-534
                               CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER:
                               Nature Publishing Group
DOCUMENT TYPE:
                               Journal
                               English
LANGUAGE:
      The mosquito-borne malaria parasite Plasmodium
      falciparum kills an estimated 0.7-2.7 million people every year,
      primarily children in sub-Saharan Africa. Without effective
      interventions, a variety of factors-including the spread of
      parasites resistant to antimalarial drugs and the increasing
      insecticide resistance of mosquitoes-may cause the number of malaria
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cases to double over the next two decades. To stimulate basic research and facilitate the development of new drugs and vaccines, the genome of Plasmodium falciparum clone 3D7 has been sequenced using a chromosome-by-chromosome shotgun strategy. This report describes nucleotide sequences of chromosomes 10, 11 and 14, and a re-anal. of the chromosome 2 sequence. These chromosomes represent about 35% of the 23-megabase P. falciparum genome. The sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AE001362.2 (chromosome 2),  $^{\sim}$  AE014185 (chromosome\_10), AE014186 (chromosome 11), and AE014187 $^{\circ}$ (chromosome 14).

ΙT 465605-54-3

> RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; complete sequence of Plasmodium

falciparum chromosomes 2, 10, 11 and 14)

30

REFERENCE COUNT:

THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 5 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

2002:485238 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 137:242895

TITLE: Comparative genomic analysis in the region of a

major Plasmodium-refractoriness locus

of Anopheles gambiae

Thomasova, Dana; Ton, Lucas Q.; Copley, Richard AUTHOR (S):

> R.; Zdobnov, Evgeny M.; Wang, Xuelan; Hong, Young S.; Sim, Cheolho; Bork, Peer; Kafatos,

Fotis C.; Collins, Frank H.

CORPORATE SOURCE: European Molecular Biology Laboratory,

Heidelberg, 69117, Germany Proceedings of the National Academy of Sciences SOURCE:

of the United States of America (2002), 99(12),

8179-8184

CODEN: PNASA6; ISSN: 0027-8424 National Academy of Sciences

PUBLISHER: DOCUMENT TYPE: Journal

LANGUAGE: English

We have sequenced six overlapping clones from a library of bacterial artificial chromosome (BAC) clones derived from a laboratory strain of the mosquito, Anopheles gambiae, the major vector of human malaria in Africa. The resulting uninterrupted 528-kb sequence is from the 8C region of the mosquito 2R chromosome, at or very near the major refractoriness locus associated with melanotic encapsulation of parasites. This sequence represents the first extensive view of the mosquito genome structure encompassing 48 genes. Genomic comparison reveals that the majority of the orthologues are found in six microsyntenic clusters in Drosophila melanogaster. A BAC clone that is wholly contained within this region demonstrates the existence of a remarkable degree of local polymorphism in this species, which may prove important for its population structure and vectorial capacity.

9000-83-3

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(V-type, sequence homolog to; comparative genomic anal. in the region of a major Plasmodium-refractoriness locus of Anopheles gambiae)

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L12 ANSWER 6 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:394971 HCAPLUS

DOCUMENT NUMBER: 135:118715

TITLE: Expression and functional characterization of a

Plasmodium falciparum Ca2+-

ATPase (PfATP4) belonging to a subclass

unique to apicomplexan organisms

AUTHOR(S): Krishna, Sanjeev; Woodrow, Charles; Webb,

Richard; Penny, Jeff; Takeyasu, Kunio; Kimura,

Masatsugu; East, J. Malcolm

CORPORATE SOURCE:

Department of Infectious Diseases, St. George's Hospital Medical School, London, SW17 ORE, UK Journal of Biological Chemistry (2001), 276(14),

SOURCE: 10782-10787

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular

Biology

DOCUMENT TYPE: Journal LANGUAGE: English

We have obtained a full-length P type ATPase sequence

(PfATP4) encoded by Plasmodium falciparum and expressed PfATP4 in Xenopus laevis oocytes to study its function.

Comparison of the hitherto incomplete open reading frame with other Ca2+-ATPase sequences reveals that PfATP4 differs

significantly from previously defined categories. The Ca2+-dependent ATPase activity of PfATP4 is

stimulated by a much broader range of [Ca2+] free (3.2-320  $\mu M)$  than are an avian SERCA1 pump or rabbit SERCA 1a (maximal activity < 10  $\mu M$ ). The activity of PfATP4 is resistant to inhibition by ouabain (200  $\mu M$ ) or thapsigargin (0.8  $\mu M$ ) but is inhibited by vanadate (1 mM) or cyclopiazonic acid (1  $\mu$ M). We used a quant. polymerase chain reaction to assay expression of mRNA encoding PfATP4 relative to that for  $\beta$ -tubulin in synchronized asexual stages and found variable expression throughout the life cycle with a maximal 5-fold increase in meronts compared with ring stages. This anal. suggests that PfATP4 defines a novel subclass of Ca2+-ATPases unique to apicomplexan organisms and therefore offers potential as a drug target.

9000-83-3, ATPase

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)

(calcium-activated, PfATP4; expression and functional characterization of a Plasmodium falciparum

Ca2+-ATPase (PfATP4) belonging to a subclass unique to

apicomplexan organisms)

REFERENCE COUNT:

THERE ARE 38 CITED REFERENCES AVAILABLE 38 FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L12 ANSWER 7 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:694055 HCAPLUS

DOCUMENT NUMBER: 121:294055

TITLE: Plasmodium falciparum:

further characterization of putative cation

**ATPases** 

Krishna, Sanjeev; Cowan, Gill M.; Robson, AUTHOR(S):

Kathryn J.; Meade, John C.

CORPORATE SOURCE: Inst. Mol. Med., John Radcliffe Hosp., Oxford,

OX3 9DU, UK

Experimental Parasitology (1994), 78(1), 113-17 SOURCE:

CODEN: EXPAAA; ISSN: 0014-4894

DOCUMENT TYPE:

Journal English LANGUAGE:

The emergence of multi-drug resistant strains of Plasmodium

falciparum and the current lack of a vaccine have stimulated research to identify new chemotherapeutic targets. The authors have focused on the isolation and

characterization of nucleotide sequences encoding putative "P"-type

cation ATPases from P. falciparum, because

selective inhibitors of mammalian members of this transporter family are well studied, and some are already in clin. use. This report describes the isolation and sequence anal. of two addnl. members of

this family, ATPases 2 and 3, and their differential

expressivity during the erythrocytic stage of parasite development. Amino acid sequence anal. identified the 7 amino acid motifs present

at the phosphorylation site (DKTGTLT) of other P-type cation

ATPases, in both clones. ATPase 2 was localized to chromosome 5 and ATPase 3 to chromosome 12 on a

Southern blot of chromosomes resolved by pulsed-field gel electrophoresis. Northern blot anal. showed that both

ATPases 2 and 3 were expressed during the erythrocytic stage of the infection. ATPase 2 has a mRNA transcript size of

5.5-6 kb and is expressed at the schizont stage of development.

ATPase 3 mRNA is approx. 5 kb in size and the strongest signal corresponds to mRNA from parasites at the ring stage of development (12-24 h postinvasion), although mRNA is also detected in all other erythrocytic stages examined

IT 9000-83-3, ATPase

RL: PRP (Properties)

(2 and 3; sequence and chromosomal localization and developmental expression of genes encoding P-type cation ATPases 2 and 3 of Plasmodium falciparum)

L12 ANSWER 8 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:407323 HCAPLUS

DOCUMENT NUMBER: 121:7323

TITLE: Immunomodulatory peptides binding to

human major histocompatibility complex (MHC)

class II allotype

INVENTOR(S): Urban, Robert Glen; Chicz, Roman M.; Vignali,

Dario A. A.; Hedley, Mary Lynne; Stern, Lawrence

J.; Strominger, Jack L.

President and Fellows of Harvard College, USA PATENT ASSIGNEE(S):

PCT Int. Appl., 59 pp. SOURCE:

CODEN: PIXXD2

DOCUMENT TYPE: ... Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

```
WO 1992-US6692
                             19940303
                                                              19920811
     WO 9404557
                       A1
         W: JP
                             19960312
                                             JP 1992-506181
                                                               19920811
     JP 08502244
PRIORITY APPLN. INFO.:
                                          WO 1992-US6692
                                                               19920811
     A purified oligopeptide preparation comprising an amino acid sequence
     identical to that of a segment of a naturally-occurring human
     protein that binds to human major histocompatibility complex
     (MHC) class II allotype is provided. The human protein is
     an MHC class I or II mol., HLA-A2, invariant chain (Ii), etc.,. A
     method is described for inhibiting an immune response in a human
     patient by contacting an antigen-presenting cell (APC) of the
     patient with a therapeutic composition or an immune-stimulating
     complex (ISCOM) containing the oligopeptide, or by expression of the
     oligopeptide-coding sequence linked to a trafficking sequence in
     APCs. The oligopeptide also can be used for inducing an immune response against pathogens. The options of the oligopeptide
     delivery system is also described. Purification and characterization of 6 HLA-DR antigens (HLA-DR1.apprx.4; HLA-DR7.apprx.8) from
     Epstein-Barr virus-transformed human B lymphoblastoid cell lines
     were demonstrated.
     9000-83-3, ATPase
IT
     RL: BIOL (Biological study)
        (Na+/K+, peptides of, as immunomodulators)
L12 ANSWER 9 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:
                          1991:673744 HCAPLUS
                          115:273744
DOCUMENT NUMBER:
                          Stimulation of the interaction between
TITLE:
                          actin and myosin by Physarum caldesmon-like
                          protein and smooth muscle caldesmon
                          Ishikawa, Ryoki; Okagaki, Tsuyoshi;
Higashi-Fujime, Sugie; Kohama, Kazuhiro
AUTHOR(S):
                          Sch. Med., Gunma Univ., Maebashi, 371, Japan
CORPORATE SOURCE:
                          Journal of Biological Chemistry (1991), 266(32),
SOURCE:
                          21784-90
                          CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE:
                          Journal
LANGUAGE:
                          English
     An actin-binding protein was purified from the
     plasmodia of a lower eukaryote, P. polycephalum, with an
     apparent mol. weight of 210 kDa on SDS-PAGE. This protein
     bound to actin filaments with a stoichiometry of 1:\overline{7}-8 in a
     Ca2+-calmodulin-dependent manner. Antibody raised against caldesmon
     from smooth muscle cross-reacted with the 210-kDa protein.
     In vitro motility assay revealed that the 210-kDa protein
     increased the sliding velocity of actin filaments on Physarum
     myosin. The 210-kDa protein more than doubled the
     actin-activated ATPase activity of Physarum myosin under
     comparative conditions of in vitro motility assay. Further
 increases in the concentration of the 210-kDa protein decreased
     its stimulatory effects. Ca2+-calmodulin prevented the
     stimulatory effects of the 210-kDa protein.
     Unexpectedly, smooth muscle caldesmon also increased the sliding
     velocity of actin filaments on smooth muscle myosin at lower concns.
     The well-known inhibitory effect of smooth muscle caldesmon on the
     actin-myosin interaction was observed with this motility assay when the
     concentration of the caldesmon was increased further. The
```

stimulatory and inhibitory effects were confirmed by measurements of actin-activated ATPase activity of smooth muscle myosin. From estns. of the intracellular concns. of the 210-kDa protein and smooth muscle caldesmon in vivo, it appears that effects of the former and the latter on actin-myosin interactions in vivo are stimulatory and inhibitory, resp.

IT 9000-83-3, ATPase

RL: BIOL (Biological study)

(of myosin, actin-binding protein of Physarum polycephalum and caldesmon of smooth muscle effect on)

L12 ANSWER 10 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

1989:3408 HCAPLUS

DOCUMENT NUMBER:

110:3408

TITLE:

Purification of Plasmodium

falciparum digestive vacuoles and

partial characterization of the vacuolar

membrane ATPase

AUTHOR(S):

SOURCE:

Choi, Inpyo; Mego, John L.

CORPORATE SOURCE:

Dep. Biol., Univ. Alabama, Tuscaloosa, AL, USA Molecular and Biochemical Parasitology (1988),

31(1), 71-8 CODEN: MBIPDP; ISSN: 0166-6851

DOCUMENT TYPE:

Journal English

LANGUAGE:

P. falciparum digestive vacuoles containing Fe3+ oxide granules were purified from parasite homogenates by centrifugation on discontinuous sucrose gradients. Digestive vacuole membranes prepared by osmotic lysis and washed with KCl showed no detectable contamination by erythrocyte membrane proteins and only minimal contamination by nonvacuolar parasite proteins. Purified vacuolar membranes were 2.6-fold enriched in total parasite membrane ATPase activity. This ATPase was optimally active at pH  $\bar{7}$  in the presence of >2 mM Mg2+. Ca2+ and Mn2+ were .apprx.80-90% as effective as Mg2+, and Zn2+, Co2+, and Fe2+ also exerted some **stimulatory** effect. The vacuolar membrane also hydrolyzed GTP, UTP, CTP, and ADP, but AMP and 3',5'-cAMP were hydrolyzed only one-tenth as effectively as ATP. The ATPase was unaffected by vanadate, ouabain, or oligomycin but was significantly inhibited by the proton pump inhibitors NEM and NBD-Cl. Of 6 antimalarial drugs tested, quinine

IT 9000-83-3P, ATPase

RL: PREP (Preparation)

the least effective.

(of digestive vacuoles of Plasmodium falciparum

, purification and characterization of)

L12 ANSWER 11 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

1982:434955 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 97:34955

A novel 36,000-dalton actin-binding protein TITLE: purified from microfilaments in Physarum

plasmodia which aggregates actin

and quinacrine were the most effective inhibitors and mefloquine was

filaments and blocks actin-myosin interaction

Ogihara, Satoshi; Tonomura, Yuji AUTHOR(S):

Fac. Sci., Osaka Univ., Osaka, 560, Japan

CORPORATE SOURCE: Journal of Cell Biology (1982), 93(3), 604-14 SOURCE:

CODEN: JCLBA3; ISSN: 0021-9525

DOCUMENT TYPE: Journal LANGUAGE: English

The plasmodia of P. polycephalum contains large aggregates AΒ of entangled actin microfilaments. Treatment with Triton X-100 gave a demembraned cytoskeleton consisting of entangled actin filaments which showed almost no interaction with rabbit skeletal myosin. A novel actin-binding protein purified from the cytoskeleton stoichiometrically binds to actin and causes actin filaments to curl and aggregate. The protein inhibits ATPase activity as well as the superpptn. of reconstituted rabbit skeletal muscle actomyosin. This protein has a mol. weight of 36,000 and binds 7 mol of actin/mol 36,000 polypeptide.

IT 9000-83-3

RL: BIOL (Biological study)

(inhibition of, of actomyosin, actin-binding protein inhibition

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 14:31:47 ON 07 OCT 2003)

3 S L8 L13 L14 21 S L10

24 S L13 OR L14 L15

L16 17 DUP REM L15 (7 DUPLICATES REMOVED)

L16 ANSWER 1 OF 17 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-505298 [47] WPIDS

DOC. NO. CPI: TITLE:

C2003-135135

New vector, useful for preparing a composition for treating or preventing bacterial, viral, fungal or

parasitic infection.

DERWENT CLASS:

B04 C06 D16

INVENTOR(S):

FRASER, W D; GALLAGHER, J A; MCCREAVY, D T

PATENT ASSIGNEE(S):

(UYLI-N) UNIV LIVERPOOL

COUNTRY COUNT:

101

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 2003048371 A2 20030612 (200347) \* EN 52

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SI SK SL SZ TR TZ UG ZM ZW W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SC SD SE SG SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO KIND APPLICATION DATE \_\_\_\_\_\_ : · \_\_\_\_\_\_\_\_ WO 2003048371 A2 WO 2002-GB5512 20021206

PRIORITY APPLN. INFO: GB 2002-23829 20021012; GB 2001-29338

20011207

2003-505298 [47] WPIDS ΔN

AB . WO2003048371 A UPAB: 20030723

NOVELTY - An vector comprising a heterologous nucleic acid sequence encoding an antigenic **polypeptide** and a nucleic acid molecule comprising a 3188 base pair sequence, given in the specification, a nucleic acid molecule which hybridizes to it and which encodes a protease inhibitor **polypeptide**, or nucleic acid molecules which comprise degenerate nucleic acid sequences. The vector is adapted for the expression of each **polypeptide**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) inducing an immune response to an antigenic polypeptide;
  - (2) an antibody;
  - (3) a cell transformed with the novel vector;
  - (4) producing humanized or chimeric antibody;
  - (5) a hybridoma cell line which produces a monoclonal antibody;
  - (6) a vaccine comprising the novel vector; and
- (7) vaccinating an animal, preferably a human, against at least one pathological condition.

ACTIVITY - Antibacterial; Virucide; Antiparasitic; Antifungal; Anti-HIV; Antiulcer.

No biological data is given.

MECHANISM OF ACTION - Gene therapy; Vaccine.

USE - The vector is useful for preparing a composition for preventing or treating AIDS, herpes, rubeola, rubella, varicella, influenza, common cold or viral meningitis; septicemia, tuberculosis, bacteria-associated food poisoning, blood infections, peritonitis, endocarditis, sepsis, bacterial meningitis, pneumonia, stomach ulcers, gonorrhea, strep throat, streptococcal-associated toxic shock, necrotizing fasciitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis, dysentery or shigellosis; Candidiasis; or trypanosomiasis, malaria, schistosomiasis or Chagas disease (claimed).

Dwg.0/9

L16 ANSWER 2 OF 17 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2003300235 EMBASE

TITLE: The pathophysiology of falciparum malaria.

AUTHOR: Clark I.A.; Cowden W.B.

CORPORATE SOURCE: I.A. Clark, Sch. of Biochem./Molecular Biology,

Australian National University, Canberra, ACT 0200,

Australia. ian.clark@anu.edu.au

SOURCE: Pharmacology and Therapeutics, (1 Aug 2003) 99/2

(221-260). Refs: 466

ISSN: 0163-7258 CODEN: PHTHDT

COUNTRY: United States

DOCUMENT TYPE: Journal; General Review FILE SEGMENT: 004 Microbiology

017 Public Health, Social Medicine and

Epidemiology

026 Immunology, Serology and Transplantation

037 Drug Literature Index 038 Adverse Reactions Titles

LANGUAGE: English SUMMARY LANGUAGE: English

AB Falciparum malaria is a complex disease with no simple

explanation, affecting organs where the parasite is rare as well as those organs where it is more common. We continue to argue that it can best be understood in terms of excessive stimulation of normally useful pathways mediated by inflammatory cytokines, the prototype being tumor necrosis factor (TNF). These pathways involve downstream mediators, such as nitric oxide (NO) that the host normally uses to control parasites, but which, when uncontrolled, have bioenergetic failure of patient tissues as their predictable end point. Falciparum malaria is no different from many other infectious diseases that are clinically confused with it. The sequestration of parasitized red blood cells, prominent in some tissues but absent in others with equal functional loss, exacerbates, but does not change, these overriding principles. Recent opportunities to stain a wide range of tissues from African pediatric cases of falciparum malaria and sepsis for the inducible NO synthase (iNOS) and migration inhibitory factor (MIF) have strengthened these arguments considerably. The recent demonstration of bioenergetic failure in tissue removed from sepsis patients being able to predict a fatal outcome fulfils a prediction of these principles, and it is plausible that this will be demonstrable in severe falciparum malaria. Understanding the disease caused by falciparum malaria at a molecular level requires an appreciation of the universality of poly(ADP-ribose) polymerase-1 (PARP-1) and Na(+)/K(+)-ATPase and the protean effects of activation by inflammation of the former that include inactivation of the latter. . COPYRGT. 2003 Elsevier Inc. All rights reserved.

L16 ANSWER 3 OF 17 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 1

ACCESSION NUMBER: 2

2003191572 EMBASE

TITLE:

SOURCE:

Replication fork-stimulated eIF-4A from

Plasmodium cynomolgi unwinds DNA in the 3' to
5' direction and is inhibited by DNA-interacting

compounds.

AUTHOR:

CORPORATE SOURCE:

Tuteja R.; Tuteja N.; Malhotra P.; Chauhan V.S. R. Tuteja, Intl. Ctr. for Genetic Eng./Biotech.,

Aruna Asaf Ali Marg, New Delhi 110067, India. renu@icgeb.res.in

Archives of Biochemistry and Biophysics, (1 Jun 2003)

414/1 (108-114).

Refs: 47

ISSN: 0003-9861 CODEN: ABBIA4

COUNTRY:
DOCUMENT TYPE:
FILE SEGMENT:

United States
Journal; Article
030 Pharmacology

030 Pharmacology 037 Drug Literature Index

LANGUAGE: English
SUMMARY LANGUAGE: English

AB Plasmodium cynomolgi DEAD-box DNA helicase 45 (PcDDH45) is an ATP-dependent DNA-unwinding enzyme with intrinsic DNA-dependent ATPase activity and is highly homologous to eIF-4A. In this study, we have further characterized and tested the effect of various DNA-interacting compounds on the DNA-unwinding activity of PcDDH45. The results show that PcDDH45 translocates in the 3' to 5' direction along the bound strand, a replication fork-like structure of the substrate stimulates its DNA-unwinding activity, and it failed to unwind blunt-ended duplex DNA. Of various compounds

tested, only cisplatin, 4',6'-diamidino-2-phenylindole, daunorubicin, and nogalamycin were inhibitory to the unwinding activity of PcDDH45 with apparent IC(50) values of 1.0, 4.0, 7.5, and 1.7 $\mu$ M, respectively. These results suggest that the interaction of these compounds with duplex DNA generate a complex that probably impedes the translocation of PcDDH45, resulting in inhibition of unwinding activity. This study is one of the first to demonstrate the effect of various DNA-binding compounds on a malaria parasite DNA helicase and should make an important contribution to our better understanding of the nucleic acid transactions in the parasite. .COPYRGT. 2003 Elsevier Science (USA). All rights reserved.

L16 ANSWER 4 OF 17 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

ACCESSION NUMBER: 2002:547065 SCISEARCH

THE GENUINE ARTICLE: 566XK

TITLE: Multidrug resistance phenotype mediated by the

P-glycoprotein-like transporter in Leishmania: A

search for reversal agents

AUTHOR: Perez-Victoria J M; Di Pietro A; Barron D; Ravelo A

G; Castanys S; Gamarro F (Reprint)

CORPORATE SOURCE: CSIC, Inst Parasitol & Biomed Lopez Neyra, C

Ventanilla 11, Granada 18001, Spain (Reprint); CSIC, Inst Parasitol & Biomed Lopez Neyra, Granada 18001, Spain; CNRS, UMR 5086, Inst Biol & Chim Prot, Lyon, France; Univ Lyon 1, CNRS, Lab Prod Nat, F-69622 Villeurbanne, France; Univ La Laguna, Inst Bioorgan

Antonio Gonzalez, Tenerife, Spain

COUNTRY OF AUTHOR:

SOURCE:

R: Spain; France

CURRENT DRUG TARGETS, (AUG 2002) Vol. 3, No. 4, pp.

311-333.

Publisher: BENTHAM SCIENCE PUBL LTD, PO BOX 1673,

1200 BR HILVERSUM, NETHERLANDS.

ISSN: 1389-4501.

DOCUMENT TYPE:

General Review; Journal

LANGUAGE: English

REFERENCE COUNT: 193
\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Protozoan parasites are responsible for important diseases that AB threaten the lives of nearly one-quarter of the human population world-wide. Among them, leishmaniasis has become the second cause of death, mainly due to the emergence of parasite resistance to conventional drugs. P-glycoprotein (Pgp)-like transporters overexpression is a very efficient mechanism to reduce the intracellular accumulation of many drugs in cancer cells and parasitic protozoans including Plasmodium and Leishmania, thus conferring a multidrug resistance (MDR) phenotype. Therefore, there is a great clinical interest in developing inhibitors of these transporters to overcome such a resistance. Pgps are active pumps belonging to the ATP-binding cassette (ABC) superfamily of proteins, and consist of two homologous halves, each containing a transmembrane domain (TMD) involved in drug efflux, and a cytosolic nucleotide-binding domain (NBD) responsible for ATP binding and hydrolysis. Most conventional cancer MDR modulators interact with the drug-binding sites on the TMDs of Pgps, but they are also usually transported and the required concentrations for a permanent inhibition produce subsequent side-effects that hamper their clinical use. Besides, they only poorly modulate the

resistance in protozoan parasites. We review here a rational strategy developed to overcome the MDR phenotype in Leishmania, consisting in: i) the selection of an MDR Leishmania tropica line that overexpresses a Pgp-like transporter; ii) the use of their cytosolic NBDs as new pharmacological targets; iii) the search of new natural compounds that revert the MDR phenotype in Leishmania by binding to the TMDs; iv) the combination of subdoses of the above selected modulators directed to both targets in the transporter, NBDs and TMDs, to accumulate their reversal effects while diminishing their toxicity. In this way, we have reverted the MDR phenotype in Leishmania, including the resistance to the most promising new antileishmania agents, the alkyl-lysophospholipids. This approach might be extrapolated to be used in other eukaryotic cells.

L16 ANSWER 5 OF 17 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS

RESERVED. on STN

ACCESSION NUMBER: 2002097347 EMBASE

TITLE: Cytoskeleton of apicomplexan parasites.

AUTHOR: Morrissette N.S.; Sibley L.D.

CORPORATE SOURCE: N.S. Morrissette, Department of Molecular

Microbiology, Washington Univ. School of Medicine, 660 South Euclid Ave., St. Louis, MO 63110, United

States. naomi@borcim.wustl.edu

SOURCE: Microbiology and Molecular Biology Reviews, (2002)

66/1 (21-38).

Refs: 200

ISSN: 1092-2172 CODEN: MMBRF7

COUNTRY: United States

DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 004 Microbiology
030 Pharmacology

037 Drug Literature Index

LANGUAGE: English SUMMARY LANGUAGE: English

The Apicomplexa are a phylum of diverse obligate intracellular parasites including Plasmodium spp., the cause of malaria; Toxoplasma gondii and Cryptosporidium parvum, opportunistic pathogens of immunocompromised individuals; and Eimeria spp. and Theileria spp., parasites of considerable agricultural importance. These protozoan parasites share distinctive morphological features, cytoskeletal organization, and modes of replication, motility, and invasion. This review summarizes our current understanding of the cytoskeletal elements, the properties of cytoskeletal proteins, and the role of the cytoskeleton in polarity, motility, invasion, and replication. We discuss the unusual properties of actin and myosin in the Apicomplexa, the highly stereotyped microtubule populations in apicomplexans, and a network of recently discovered novel intermediate filament-like elements in these parasites.

L16 ANSWER 6 OF 17 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 2001560947 MEDLINE

DOCUMENT NUMBER: 21519010 PubMed ID: 11606229

TITLE: Microtubule associated motor proteins of

Plasmodium falciparum merozoites.

AUTHOR: Fowler R E; Smith A M; Whitehorn J; Williams I T;

Bannister L H; Mitchell G H

CORPORATE SOURCE: Malaria Laboratory, Department of Immunobiology,

Guy's, King's and St Thomas' School of Medicine, KCL, Guy's Hospital, London Bridge, London, SE1 9RT, UK...

ruth.fowler@ed.ac.uk

MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2001 Oct) SOURCE:

117 (2) 187-200.

Journal code: 8006324. ISSN: 0166-6851.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200201

ENTRY DATE: Entered STN: 20011022

> Last Updated on STN: 20020201 Entered Medline: 20020131

AB We have studied the occurrence, stage specificity and cellular location of key molecules associated with microtubules in

Plasmodium falciparum merozoites. Antibodies to

gamma tubulin, conventional kinesin and cytoplasmic dynein were used to determine the polarity of merozoite microtubules (mt), the stage specificity of the motor proteins and their location during merozoite development. We conclude that the minus ends of the mts are located at their apical pole. Kinesin was present throughout the lifecycle, appearing as a distinct crescent at the apex of developing merozoites. The vast majority of cytoplasmic dynein reactivity occurred in late merogony, also appearing at the merozoite apex. Destruction of mt with dinitroanilines did not affect the cellular location of kinesin or dynein. In invasion assays, dynein inhibitors reduced the number of ring stage parasites. Our results show that both conventional kinesin and cytoplasmic dynein are abundant, located at the negative pole of the merozoite mt and, intriguingly, appear there only in very late merogony, prior to merozoite release and invasion.

L16 ANSWER 7 OF 17 MEDLINE on STN ACCESSION NUMBER: 2001297917 MEDLINE

DOCUMENT NUMBER: 21273137 PubMed ID: 11378198

TITLE: Two classes of plant-like vacuolar-type

H(+)-pyrophosphatases in malaria parasites.

AUTHOR: McIntosh M T; Drozdowicz Y M; Laroiya K; Rea P A;

Vaidya A B

Department of Microbiology and Immunology, MCP CORPORATE SOURCE:

Hahnemann University, 2900 Queen Lane, Philadelphia,

PA 19129, USA.. michael.t.mcintosh@drexel.edu

CONTRACT NUMBER: AF28398

SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2001 May)

114 (2) 183-95.

Journal code: 8006324. ISSN: 0166-6851.

PUB. COUNTRY:

Netherlands

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

GENBANK-AF115766; GENBANK-AF115767; GENBANK-AF283528 OTHER SOURCE:

ENTRY MONTH: 200108

Entered STN: 20010806 ENTRY DATE:

Last Updated on STN: 20010806 Entered Medline: 20010802

AB In plants, cytosolic inorganic pyrophosphate (PP(i)) is hydrolyzed by energy-conserving vacuolar-type H(+)-pyrophosphatases (V-PPases)

that harness the free energy of PP(i) hydrolysis to establish transmembrane H(+) gradients. Here we describe the identification and cloning of two genes, PfVP1 and PfVP2, from the malaria parasite Plasmodium falciparum. Inferred to encode type I (K(+)-dependent) and type II (K(+)-independent) V-PPases, respectively, PfVP1 and PfVP2 appeared more sequence divergent from each other than from their type I and type II counterparts in The steady state levels of PfVP1 mRNA were high in comparison to PfVP2 mRNA throughout the erythrocytic phases of infection. Western analyses of trophozoite membranes using generic V-PPase antibodies (PAB(HK) and PAB(TK)) demonstrated appreciable amounts of a Mr 67000 polypeptide whose associated aminomethylenediphosphonate- (AMDP) inhibitable PPase activity was markedly **stimulated** by K(+). Immunofluorescence microscopy of infected erythrocytes revealed PfVP antigen associated with both the parasite plasma membrane and punctate intracellular inclusions. Transient transfection of a PfVP1-GFP fusion further supported the localization of PfVP1 to the parasite plasma membrane. Based on these findings and the growth-retarding effects of AMDP, P. falciparum is concluded to possess both type I and type II V-PPases of which the former has the greatest potential for contributing to the establishment of H(+) gradients across the parasite plasma membrane under conditions of energy limitation.

L16 ANSWER 8 OF 17 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN ACCESSION NUMBER: 2001:373496 SCISEARCH

THE GENUINE ARTICLE: 427QR

TITLE: Detection and localization of a Ca2+-ATPase

activity in Toxoplasma gondii

AUTHOR: Bouchot A; Jaillet J D; Bonhomme A (Reprint);

Pezzella-D'Alessandro N; Laquerriere P; Kilian L; Burlet H; Gomez-Marin J E; Pluot M; Bonhomme P;

Pinon J M

CORPORATE SOURCE: CHU Maison Blanche, IFR 53, UPRES EA 2070, 51 Rue

Cognacq Jay, F-51095 Reims, France (Reprint); CHU Maison Blanche, IFR 53, UPRES EA 2070, F-51095 Reims, France; CHU Maison Blanche, IFR 53, Lab

Parasitol Mycol, F-51095 Reims, France; Lab

Microscopie Elect Analyt & Quantitat, IFR 53, Reims, France; Hop Robert Debre, Anat Pathol Lab, Reims, France; Univ Nacl Colombia, Hosp San Juan de Dios, Dept Med Interna, Grp Pathol Infecciosa, Santafe De

Bogota, Colombia

COUNTRY OF AUTHOR:

France; Colombia

SOURCE:

CELL STRUCTURE AND FUNCTION, (FEB 2001) Vol. 26, No.

1, pp. 49-60.

Publisher: JAPAN SOC CELL BIOLOGY, SHIMOTACHIURI OGAWA-HIGASHI, KAMIKYOKU KYOTO, 602, JAPAN.

ISSN: 0386-7196.

DOCUMENT TYPE:

Article; Journal

LANGUAGE:

English

REFERENCE COUNT: 59

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Toxoplasma gondii, the agent causing toxoplasmosis, is an obligate intracellular protozoan parasite. A calcium signal appears to be essential for intracellular transduction during the active process of host cell invasion. We have looked for a Ca2+-transport ATPase in tachyzoites and found Ca2+-ATPase

activity (11-22 nmol Pi liberated/mg protein/min) in the tachyzoite membrane fraction, This ATP-dependent activity was stimulated by Ca2+ and Mg2+ ions and by calmodulin, and was inhibited by pomp inhibitors (sodium orthovanadate or thapsigargin). We used cytochemistry and X-ray microanalysis of cerium phosphate precipitates and immunolabelling to find the Ca2+, Mg2+-ATPase. It was located mainly in the membrane complex, the conoid, nucleus, secretory organelles (rhoptries, dense granules) and in vesicles with a high calcium concentration, Thus, Toxoplasma gondii possesses Ca2+-pump ATPase (Ca2+, Mg2+-ATPase) as do eukaryotic cells.

L16 ANSWER 9 OF 17 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

ACCESSION NUMBER: 2000:622594 SCISEARCH

THE GENUINE ARTICLE: 343QA

TITLE: Vacuolar proton pyrophosphatase activity and

pyrophosphate (PPi) in Toxoplasma gondii as possible

chemotherapeutic targets

AUTHOR: Rodrigues C O; Scott D A; Bailey B N; deSouza W;

Benchimol M; Moreno B; Urbina J A; Oldfield E;

Moreno S N J (Reprint)

CORPORATE SOURCE: UNIV ILLINOIS, COLL VET MED, DEPT PATHOBIOL, MOL

PARASITOL LAB, 2001 S LINCOLN AVE, URBANA, IL 61802

(Reprint); UNIV ILLINOIS, COLL VET MED, DEPT

PATHOBIOL, MOL PARASITOL LAB, URBANA, IL 61802; UNIV

ILLINOIS, DEPT CHEM, URBANA, IL 61801; UNIV

ILLINOIS, DEPT BIOPHYS, URBANA, IL 61801; UNIV SANTA URSULA, RIO JANEIRO, BRAZIL; INST VENEZOLANO INVEST CIENT, CARACAS, VENEZUELA; UNIV FED RIO DE JANEIRO,

INST BIOFIS CARLOS CHAGAS FILHO, BR-21941 RIO

JANEIRO, BRAZIL

COUNTRY OF AUTHOR:

USA; BRAZIL; VENEZUELA

SOURCE:

BIOCHEMICAL JOURNAL, (1 AUG 2000) Vol. 349, Part 3,

pp. 737-745.

Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON

W1N 3AJ, ENGLAND. ISSN: 0264-6021.

DOCUMENT TYPE:

Article; Journal

FILE SEGMENT: LIFE LANGUAGE: Engl:

REFERENCE COUNT:

English 50

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

The addition of PPi promoted the acidification of a subcellular AΒ compartment in cell homogenates of Toxoplasma gondii tachyzoites, implying the presence of a proton-translocating pyrophosphatase. The proton gradient was collapsed by addition of the K+/H+ antiporter nigericin, and was also inhibited by addition of the PP, analogue aminomethylenediphosphonate (AMDP). Both proton transport and PPi hydrolysis were dependent upon K+, but Na+ caused partial inhibition of these activities. PPi hydrolysis was sensitive in a dose-dependent manner to AMDP, imidodiphosphate, NaF and to the thiol reagent N-ethylmaleimide. This activity was unaffected by common inhibitors of phosphohydrolases, except that NaO3V (sodium orthovanadate) stimulated the activity by 87%. Immunofluorescence microscopy, using antisera raised against conserved peptide sequences of a plant vacuolar pyrophosphatase, suggested that the pyrophosphatase in T. gondii tachyzoites was located in the plasma membrane and intracellular

vacuoles of the parasite. High-field P-31-NMR spectroscopy showed that PPi was more abundant than ATP in tachyzoites. Bisphosphonates (PPi analogues), drugs that are used in the treatment of bone diseases, inhibited proton transport and PPi hydrolysis in tachyzoite homogenates, and also inhibited intracellular proliferation of tachyzoites in tissue culture cells.

L16 ANSWER 10 OF 17 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

ACCESSION NUMBER: 2000:385352 SCISEARCH

THE GENUINE ARTICLE: 314FV

TITLE: AVP2, a sequence-divergent, K+-insensitive

H+-translocating inorganic pyrophosphatase from

arabidopsis

AUTHOR: Drozdowicz Y M; Kissinger J C; Rea P A (Reprint)
CORPORATE SOURCE: UNIV PENN, DEPT BIOL, INST PLANT SCI, PHILADELPHIA,

PA 19104 (Reprint); UNIV PENN, DEPT BIOL, INST PLANT

SCI, PHILADELPHIA, PA 19104

COUNTRY OF AUTHOR: USA

SOURCE: PLANT PHYSIOLOGY, (MAY 2000) Vol. 123, No. 1, pp.

353-362.

Publisher: AMER SOC PLANT PHYSIOLOGISTS, 15501

MONONA DRIVE, ROCKVILLE, MD 20855.

ISSN: 0032-0889.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE; AGRI LANGUAGE: English

REFERENCE COUNT: 42

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Plant vacuolar H+-translocating inorganic pyrophosphatases AB (V-PPases; EC 3.6.1.1) have been considered to constitute a family of functionally and structurally monotonous intrinsic membrane proteins. Typified by AVP1 (V. Sarafian, Y. Kim, R.J. Poole, P.A. Rea [1992] Proc Natl Acad Sci USA 89: 1775-1779) from Arabidopsis, all characterized plant V-PPases share greater than 84% sequence identity and catalyze K+-stimulated H+ translocation. Here we describe the molecular and biochemical characterization of AVP2 (accession number AF182813), a sequence-divergent (36% identical) K+-insensitive, Ca2+-hypersensitive V-PPase active in both inorganic pyrophosphate hydrolysis and H+ translocation. The differences between AVP2 and AVP1 provide the first indication that plant V-PPases from the same organism fall into two distinct categories. Phylogenetic analyses of these and other V-PPase sequences extend this principle by showing that AVP2, rather than being an isoform of AVP1, is but one representative of a novel category of AVP2-like (type II) V-PPases that coexist with AVP1-like (type I) V-PPases not only in plants, but also in apicomplexan protists such as the malarial parasite Plasmodium falciparum.

L16 ANSWER 11 OF 17 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN DUPLICATE 3

ACCESSION NUMBER: 96:116360 SCISEARCH

THE GENUINE ARTICLE: TT475

TITLE: ISOLATION AND CHARACTERIZATION OF SEA SPONGE MYOSIN AUTHOR: KANZAWA N (Reprint); TAKANOOHMURO H; MARUYAMA K CORPORATE SOURCE: CHIBA UNIV, FAC SCI, DEPT BIOL, CHIBA 263, JAPAN

(Reprint); UNIV TOKYO, FAC MED, DEPT PHARMACOL,

TOKYO 113, JAPAN

Searcher: Shears 308-4994

COUNTRY OF AUTHOR: JAPAN

ZOOLOGICAL SCIENCE, (DEC 1995) Vol. 12, No. 6, pp. SOURCE:

765-769.

ISSN: 0289-0003. Article; Journal DOCUMENT TYPE:

LIFE; AGRI FILE SEGMENT: LANGUAGE: ENGLISH

REFERENCE COUNT: 17

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Myosin was purified to a homogeneity from sea sponge, AB Halichondria okadai. The myosin consisted of 220 kDa heavy chain, 18 kDa calcium binding light chain and 21 kDa phosphorylatable light chain. Rotary shadowed images showed the two headed myosin ( myosin II) with a 160 nm tail. The myosin was less soluble in a KCl solution as compared to rabbit skeletal myosin.

The K+-stimulated and Ca2+-stimulated ATPase activities of sea sponge myosin were 0.46 and 0.07 mu mol Pi min(-1) mg(-1), respectively. The Mg2+ activated myosin ATPase activity showed no significant enhancement by the addition of rabbit skeletal muscle actin despite that the light chain was phosphorylated by myosin light chain kinase from chicken gizzard. Sea sponge myosin 18 kDa light chain bound to Ca2+ ion but was not phosphorylated like Physarum plasmodia myosin light chains.

L16 ANSWER 12 OF 17 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

95:282492 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: QT916

DRUG-STIMULATED ATPASE ACTIVITY TITLE:

OF THE HUMAN P-GLYCOPROTEIN

SCARBOROUGH G A (Reprint) AUTHOR:

UNIV N CAROLINA, DEPT PHARMACOL, CHAPEL HILL, NC, CORPORATE SOURCE:

27599 (Reprint)

COUNTRY OF AUTHOR: USA

)

AΒ

JOURNAL OF BIOENERGETICS AND BIOMEMBRANES, (FEB 1995 SOURCE:

Vol. 27, No. 1, pp. 37-41.

ISSN: 0145-479X.

General Review; Journal DOCUMENT TYPE:

FILE SEGMENT: LIFE LANGUAGE: ENGLISH

REFERENCE COUNT: 41

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

The human multidrug resistance protein, or P-glycoprotein (Pgp), exhibits a high-capacity drug-dependent ATP hydrolytic activity that is a direct reflection of its drug transport capability. This activity is readily measured in membranes isolated from cultured insect cells infected with a baculovirus

carrying the human mdrl cDNA. The drug-stimulated

ATPase activity is a useful alternative to conventional screening systems for identifying high-affinity drug substrates of the Pgp with potential clinical value as chemosensitizers for tumor cells that have become drug resistant. Using this assay system, a variety of drugs have been directly shown to interact with the Pgp.

Many of the drugs stimulate the Pgp ATPase activity, but certain drugs bind tightly to the drug-binding site of the Pgp without eliciting ATP hydrolysis. Either class of drugs may be useful as chemosensitizing agents. The baculovirus/insect cell Pgp ATPase assay system may also facilitate future studies

308-4994 Searcher : Shears

of the molecular structure and mechanism of the Pgp.

L16 ANSWER 13 OF 17 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on

STN

ACCESSION NUMBER: 1993:346268 BIOSIS DOCUMENT NUMBER: PREV199396043268

TITLE: Absence of transitory (Ca-2+)-i flux during early in

vitro metacyclogenesis of Trypanosoma cruzi.

AUTHOR(S): Krassner, Stuart M. (1); Chang, Johnny; Pak, Sung;

Luc, Kim-Oanh; Granger, Barbara

CORPORATE SOURCE: (1) Dep. Dev. Cell Biol., Univ. Calif., Irvine, CA

92717 USA

SOURCE: Journal of Eukaryotic Microbiology, (1993) Vol. 40,

No. 2, pp. 224-230. ISSN: 1066-5234.

DOCUMENT TYPE: Article

LANGUAGE: Article English

AB The phorbol ester TPA (phorbol 12-myristate 13-acetate) substitutes

for CO-2 as an agonist for transforming Trypanosoma cruzi

epimastigotes to the metacyclic trypomastigote stage in a starvation medium consisting of phosphate buffered saline + 10 mM proline, 10 mM sodium acetate and 0.035% NaHCO-3. Since TPA is thought to

stimulate protein kinase C by mimicking the

activity of the secondary messenger diacylglycerol, the above result suggested that T. cruzi metacyclogenesis could be activated by a

Ca-2+-dependent **protein** kinase C signal induction pathway.

Accordingly, cytosolic calcium Bux ((Ca-2+)-i) in epimastigotes, activated with 5% CO-2 or TPA (10-7 M), was measured with the Ca-2+ molecular probe, fluo-3AM. In addition, (Ca-2+)-i was measured in cells incubated with putative metacyclogenic agonists (e.g. proline, glutamate, bioamines, ionophores and catecholamines). None of the compounds studied, except for EGTA, affected cytosolic Ca-2+ levels.

Control assays with 11 mu-M thapsigargin, which mobilizes noncytoplasmic Ca-2+ stores by inhibiting endoplasmic reticulum Ca-2+-ATPase, validated our fluorometric assay procedure.

Although thapsigargin significantly increases cytoplasmic Ca-2+ fluorescence, it has no effect on transformation. The

protein kinase C inhibitors staurosporine, H-7 and HA 1004 were tested for their effect on T. cruzi metacyclogenesis. Low concentrations of staurosporine and HA 1004 significantly elevated Peru strain transformation while H-7 had no effect on Peru strain metacyclogenesis. Inhibitor H-7 did significantly depress CL

transformation. The results indicate that induction of T. cruzi metacyclic trypomastigote formation by CO-2 and TPA is not accompanied by changes in cytosolic Ca-2+ and do not provide supporting evidence for participation of a **protein** kinase C-mediated phosphoinositide cascade in metacyclogenesis.

L16 ANSWER 14 OF 17 MEDLINE on STN DUPLICATE 4

ACCESSION NUMBER: 92042085 MEDLINE

DOCUMENT NUMBER: 92042085 PubMed ID: 1834662

TITLE: Stimulation of the interaction between

actin and myosin by Physarum caldesmon-like

protein and smooth muscle caldesmon.

AUTHOR: Ishikawa R; Okagaki T; Higashi-Fujime S; Kohama K CORPORATE SOURCE: Department of Pharmacology, Gunma University School

of Medicine, Japan.

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Nov 15) 266

Searcher: Shears 308-4994

(32) 21784-90.

Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY:

United States

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199112

ENTRY DATE:

Entered STN: 19920124

Last Updated on STN: 19970203 Entered Medline: 19911223

We have purified an actin-binding protein from the AB plasmodia of a lower eukaryote, Physarum polycephalum, with an apparent molecular mass of 210,000 daltons on sodium dodecyl sulfate-polyacrylamide gel electrophoresis. This protein bound to actin filaments with a stoichiometry of 1:7-8 in a Ca(2+)-calmodulin-dependent manner. Antibody raised against caldesmon from smooth muscle cross-reacted with the 210-kDa protein. In vitro motility assay revealed that the 210-kDa protein increased the sliding velocity of actin filaments on Physarum myosin. The 210-kDa protein more than doubled the actin-activated ATPase activity of Physarum myosin under comparative conditions of in vitro motility assay. Further increases in the concentration of the 210-kDa protein decreased its stimulatory effects. Ca(2+)-calmodulin prevented the stimulatory effects of the 210-kDa protein. Unexpectedly, smooth muscle caldesmon also increased the sliding velocity of actin filaments on smooth muscle myosin at lower concentrations. The well-known inhibitory effect of smooth muscle caldesmon on the actin-myosin interaction was observed with this motility assay when the concentration of the caldesmon was increased further. The stimulatory and inhibitory effects were confirmed by measurements of actin-activated ATPase activity of smooth muscle myosin. From estimations of the intracellular concentrations of the 210-kDa protein and smooth muscle caldesmon in vivo, it appears that effects of the former and the latter on actin-myosin interactions in vivo are stimulatory and inhibitory, respectively.

L16 ANSWER 15 OF 17 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

ACCESSION NUMBER:

91:631866 SCISEARCH

THE GENUINE ARTICLE: GP804

TITLE:

STIMULATION OF THE INTERACTION BETWEEN

ACTIN AND MYOSIN BY PHYSARUM CALDESMON-LIKE

PROTEIN AND SMOOTH-MUSCLE CALDESMON

AUTHOR:

ISHIKAWA R (Reprint); OKAGAKI T; HIGASHIFUJIME S;

CORPORATE SOURCE:

KOHAMA K GUNMA UNIV, SCH MED, DEPT PHARMACOL, MAEBASHI, GUNMA

371, JAPAN (Reprint); NIHON UNIV, PHYS SCI LABS, FUNABASHI, CHIBA 274, JAPAN; NAGOYA UNIV, FAC SCI,

DEPT MOLEC BIOL, NAGOYA, AICHI 464, JAPAN

COUNTRY OF AUTHOR:

SOURCE:

**JAPAN** JOURNAL OF BIOLOGICAL CHEMISTRY, (1991) Vol. 266,

No. 32, pp. 21784-21790.

DOCUMENT TYPE:

Article; Journal

FILE SEGMENT:

LIFE ENGLISH

LANGUAGE: REFERENCE COUNT:

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Searcher : Shears 308-4994

AB We have purified an actin-binding protein from the plasmodia of a lower eukaryote, Physarum polycephalum, with an apparent molecular mass of 210,000 daltons on sodium dodecyl sulfate-polyacrylamide gel electrophoresis. This protein bound to actin filaments with a stoichiometry of 1:7-8 in a Ca2+-calmodulin-dependent manner. Antibody raised against caldesmon from smooth muscle cross-reacted with the 210-kDa protein. In vitro motility assay revealed that the 210-kDa protein increased the sliding velocity of actin filaments on Physarum myosin. The 210-kDa protein more than doubled the actin-activated ATPase activity of Physarum myosin under comparative conditions of in vitro motility assay. Further increases in the concentration of the 210-kDa protein decreased its stimulatory effects. Ca2+-calmodulin prevented the stimulatory effects of the 210-kDa protein. Unexpectedly, smooth muscle caldesmon also increased the sliding velocity of actin filaments on smooth muscle myosin at lower concentrations. The well-known inhibitory effect of smooth muscle caldesmon on the actin-myosin interaction was observed with this motility assay when the concentration of the caldesmon was increased further. The stimulatory and inhibitory effects were confirmed by measurements of actin-activated ATPase activity of smooth muscle myosin. From estimations of the intracellular concentrations of the 210-kDa protein and smooth muscle caldesmon in vivo, it appears that effects of the former and the latter on actin-myosin interactions in vivo are stimulatory and inhibitory, respectively.

L16 ANSWER 16 OF 17 MEDLINE on STN DUPLICATE 5

ACCESSION NUMBER:

89040035

MEDLINE

DOCUMENT NUMBER:

89040035 PubMed ID: 2972931

TITLE:

Purification of **Plasmodium** 

falciparum digestive vacuoles and partial
characterization of the vacuolar membrane

ATPase.

AUTHOR:

Choi I; Mego J L

CORPORATE SOURCE:

Department of Biology, University of Alabama,

Tuscaloosa 35487.

SOURCE:

MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1988 Oct) 31

(1) 71-8.

Journal code: 8006324. ISSN: 0166-6851.

PUB. COUNTRY:

Netherlands

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

198812

ENTRY DATE:

Entered STN: 19900308

Last Updated on STN: 19900308 Entered Medline: 19881220

AB Plasmodium falciparum digestive vacuoles

containing ferric oxide granules were purified from parasite homogenates by centrifugation on discontinuous sucrose gradients. Digestive vacuole membranes prepared by osmotic lysis and washed with KCl showed no detectable contamination by erythrocyte membrane proteins and only minimal contamination by non-vacuolar parasite proteins. Purified vacuolar membranes were 2.6-fold enriched in total parasite membrane ATPase activity. This ATPase was optimally active at pH 7 in the

Searcher: Shears 308-4994

presence of at least 2 mM Mg2+. Ca2+ and Mn2+ were approximately 80-90% as effective as Mg2+, and Zn2+, Co2+ and Fe2+ also exerted some **stimulatory** effect. The vacuolar membrane also hydrolyzed GTP, UTP, CTP and ADP, but AMP and 3',5'-cyclic AMP were hydrolyzed only one-tenth as effectively as ATP. The **ATPase** was unaffected by vanadate, ouabain or oligomycin but was significantly inhibited by the proton pump inhibitors NEM and NBD-Cl. Of 6 antimalarial drugs tested, quinine and quinacrine were the most effective inhibitors and mefloquine was the least effective.

L16 ANSWER 17 OF 17 EMBASE COPYRIGHT 2003 ELSEVIER INC. ALL RIGHTS

RESERVED. on STN

ACCESSION NUMBER: 74138989 EMBASE

DOCUMENT NUMBER: 1974138989

TITLE: The biosynthesis of plasmodial myosin during

starvation of Physarum polycephalum.

AUTHOR: White F.H.; Lascelles J.

CORPORATE SOURCE: Dept. Bacteriol., Univ. California, Los Angeles,

Calif. 90025, United States

SOURCE: Biochemical Journal, (1973) 135/4 (639-647).

CODEN: BIJOAK

DOCUMENT TYPE: Journal

FILE SEGMENT: 029 Clinical Biochemistry

LANGUAGE: English

AB The actomyosin protein complex of Physarum polycephalum was prepared from vegetative and starved plasmodia. The yield of actomyosin per unit wet wt was the same from both types of plasmodia. Myosin was resolved from the complex by gel filtration and purified by ion exchange chromatography. The Ca2+

stimulated adenosine triphosphatase
activities of myosin preparations from vegetative and starved
plasmodia were not appreciably different. Synthesis of
myosin de novo was shown to occur during the starvation phase of the
life cycle by the isolation of labelled myosin preparations from
plasmodia starved in the presence of [2 14C]glycine.
Fractionation of polyacrylamide gels after gel filtration of
labelled myosin confirmed the presence of label in the
adenosine triphosphatase active myosin band. It is
concluded that during starvation myosin synthesis continues although
there is a net loss of approx. 50% of the total protein.
Sodium dodecyl sulphate polyacrylamide gel electrophoresis of
Physarum myosin showed the presence of low molecular weight
components of the molecule, similar to those of muscle myosins. The
content and composition of the free amino acid pool to Physarum was

(FILE 'MEDLINE' ENTERED AT 14:43:41 ON 07 OCT 2003)
12195 SEA FILE=MEDLINE ABB=ON PLU=ON "PLASMODIUM FALCIPARUM"/

CT L30 28410 SEA FILE=MEDLINE ABB=ON PLU=ON ADENOSINETRIPHOSPHATASE/

measured at various time intervals during the vegetative and

L31 17 SEA FILE=MEDLINE ABB=ON PLU=ON L29 AND L30

L31 ANSWER 1 OF 17 MEDLINE on STN

starvation phases of the life cycle.

AN 2002675294 MEDLINE

L29

TI Transport processes in Plasmodium falciparum-infected erythrocytes:

Searcher: Shears 308-4994

- potential as new drug targets.
- AU Krishna Sanjeev; Eckstein-Ludwig Ursula; Joet Thierry; Uhlemann Anne-Catrin; Morin Christophe; Webb Richard; Woodrow Charles; Kun Jurgen F J; Kremsner Peter G
- SO INTERNATIONAL JOURNAL FOR PARASITOLOGY, (2002 Dec 4) 32 (13) 1567-73. Ref: 39 Journal code: 0314024. ISSN: 0020-7519.
- Plasmodium falciparum infection induces alterations in the transport properties of infected erythrocytes that have recently been defined using electrophysiological techniques. Mechanisms responsible for transport of substrates into intraerythrocytic parasites have also been clarified by studies of three substrate-specific (hexose, nucleoside and aquaglyceroporin) parasite plasma membrane transporters. These have been characterised functionally using the Xenopus laevis oocyte heterologous expression system. The same expression system is currently being used to define the function of parasite 'P' type ATPases responsible for intraparasitic [Ca(2+)] homeostasis. We review studies on these transport processes and examine their potential as novel drug targets.
- L31 ANSWER 2 OF 17 MEDLINE on STN
- AN 2001479314 MEDLINE
- TI Characterization of P-type ATPase 3 in Plasmodium falciparum.
- AU Rozmajzl P J; Kimura M; Woodrow C J; Krishna S; Meade J C
- SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2001 Sep 3) 116 (2) 117-26. Journal code: 8006324. ISSN: 0166-6851.
- We report the nucleotide sequence, derived amino acid sequence and AB expression profile of P-type ATPase 3 (PfATPase3) from Plasmodium falciparum. An open reading frame of 7362 nucleotides, interrupted by a single intron of 168 nt, encoded a protein product of 2394 amino acids with a predicted MW of 282791 Da. Hydropathy analysis of PfATPase3 revealed six amino-terminal and six carboxyl-terminal membrane spanning regions (M1-12) flanking a large hydrophilic domain with a smaller hydrophilic loop between M4 and M5. Based on a phylogenetic comparison of conserved domains present in P-type ATPases from other organisms, PfATPase3 resembled a Type-V ATPase for which the transport affinity is unknown. The PfATPase3 topology was interrupted by four regions, termed 'inserts', unique to malarial P-type ATPases, which were high in asparagine residues and charged amino acids (inserts I1-I4). Inserts I1 and I3 also contained repeated amino acid motifs. The number and composition of repeated amino acid motifs in insert I3 were variable in seven P. falciparum strains tested. PfATPase3 was 80.2% similar to the non-insert portions of P. yoelii ATPase3, although their inserts differed in length and composition. PfATPase3 mRNA was most abundant relative to beta-tubulin during the latter half of the erythrocytic cycle and was also present in gametocytes. Using affinity-purified antibody to a 14 amino acid PfATPase3 epitope, a 260 kDa protein was detected by Western analysis. Based on immunofluorescence, the PfATPase3 protein was located intracellularly in gametocytes and, to a lesser extent, in late erythrocytic stages.
- L31 ANSWER 3 OF 17 MEDLINE on STN
- AN 2000386953 MEDLINE
- TI Molecular cloning of a gene encoding a 20S proteasome beta subunit from Plasmodium falciparum.
- AU Li G D; Li J L; Mugthin M; Ward S A

- SO INTERNATIONAL JOURNAL FOR PARASITOLOGY, (2000 May) 30 (6) 729-33. Journal code: 0314024. ISSN: 0020-7519.
- AB A novel gene was cloned from Plasmodium falciparum. Database searches indicated this gene to be a member of the 20S proteasome beta-subunit family. Comparison of the gene's genomic DNA sequence with cDNA sequence revealed a 156-bp intron 85 bp downstream from the start codon. The nucleotide sequence of the gene contains one open reading frame encoding 265 amino acids with a predicted molecular mass of 30.9 kDa and a pI of 6.2. Northern blot analysis showed the transcript size to be approximately 1.6 kb indicating that some 800 bp of the transcript is non-coding.
- L31 ANSWER 4 OF 17 MEDLINE on STN
- AN 2000002518 MEDLINE
- TI Cloning and partial characterization of the proteasome S4 ATPase from Plasmodium falciparum.
- AU Certad G; Abrahem A; Georges E
- SO EXPERIMENTAL PARASITOLOGY, (1999 Nov) 93 (3) 123-31. Journal code: 0370713. ISSN: 0014-4894.
- AΒ Certad, G., Abrahem, A., and Georges, E. 1999. Cloning and Partial characterization of the proteasome S4 ATPase from Plasmodium falciparum. Experimental Parasitology 93, 123-131. ATP-ubiquitin-proteasome pathway mediates the nonlysosomal degradation of cytosolic proteins in eukaryotic cells. The activities of this pathway have been shown to regulate cell growth and differentiation through modulation of regulatory proteins. The proteasome is a large complex consisting of two multisubunit structures, the 20S and 19S(PA700) or P28 complexes, that combine to form the 26S particles. In this study, we describe the cloning of a cDNA encoding the proteasome subunit 4 ATPase homologue from Plasmodium falciparum (PFS4). Analysis of the PFS4 cDNA sequence shows an open reading frame encoding a deduced protein of 455 amino acids. Moreover, comparison of PFS4 cDNA sequence to that of genomic fragments encoding PFS4 showed identical sequences with no detectable introns. Database searches revealed a high sequence identity to those of rice, yeast, mouse, Drosophila, and human S4 ATPases. However, PFS4 contains two unique inserts of nine and seven amino acid residues in the N-terminal domain. Interestingly, only the rice S4 contains the latter (seven amino acids) insert with four identical amino acids. In vitro expression of the full-length cDNA encoding the PFS4, using a transcription-translation-coupled reticulocyte lysate, shows a 50-kDa [(35)S]methionine-labeled protein which was immunoprecipitated with PFS4 anti-peptide antiserum. Southern blot analysis of genomic DNA digests shows a single gene copy of PFS4 in P. falciparum. Of interest was the effect of the proteasome-specific natural product, lactacystin, on the growth of the parasite, with IC(50) values of 0.6-0.92 microM. The latter IC(50) values of lactacystin for different clones of P. falciparum are comparable to those obtained for mammalian cell lines (0.65 microM), suggesting the presence of a conserved proteasome complex. Moreover, lactacystin was equally toxic to drug-sensitive and resistant parasites. Copyright 1999 Academic Press.
- L31 ANSWER 5 OF 17 MEDLINE on STN
- AN 97418800 MEDLINE
- TI A Plasmodium falciparum homologue of the ATPase subunit of a multi-protein complex involved in chromatin remodelling for

Searcher: Shears 308-4994

transcription.

- AU Ji D D; Arnot D E
- SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1997 Sep) 88 (1-2) 151-62. Journal code: 8006324. ISSN: 0166-6851.
- AB A Plasmodium falciparum homologue of one of the components of a chromatin-remodelling complex which controls binding of transcription factors to nucleosome core particles has been cloned and characterised. The gene encodes 1422 amino acids with an estimated molecular mass of 167 kDa. The protein, SNF2L, shares 60% amino acid identity in its conserved DNA-dependent ATPase domain with yeast transcription factors originally identified by characterising mating type switch mutants. It also contains sequences related to the so-called SWI3, ADA2, N-CoR and TFIIIB B" or SANT DNA binding domains which are characteristic of these transcriptional activation factors. The SNF2L gene has two short introns in the 3' region of the coding sequence of the gene and is transcribed into a single approximately 6.5 kb messenger RNA species which is present throughout the asexual stages of the cell cycle. Southern blotting and pulsed field gel electrophoresis experiments show that SNF2L is a single copy gene. located on P. falciparum chromosome 11.
- L31 ANSWER 6 OF 17 MEDLINE on STN
- AN 96408665 MEDLINE
- TI Analysis of a cation-transporting ATPase of Plasmodium falciparum.
- AU Dyer M; Jackson M; McWhinney C; Zhao G; Mikkelsen R
- SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1996 Jun) 78 (1-2) 1-12. Journal code: 8006324. ISSN: 0166-6851.
- We have cloned and characterised one gene, PfATPase4 which encodes a AB P-type ATPase containing all the primary sequence motifs characteristic of this class of transmembrane ion transporters, and also a fragment of a second P. falciparum P-type ATPase pseudogene (PfATPase5). Analysis of conserved domains and motifs of specific ATPases reveals that PfATPase4 is most analogous to Ca2+ ATPases of the endoplasmic reticulum. The PfATPase4 gene gives rise to a transcript of 8 kb shortly after erythrocyte invasion. Although this mRNA is not detected in later stages, the protein detected immunologically at 190 kDa persists throughout and is detected in free merozoites. Immunofluorescence microscopy reveals that the PfATPase4 protein is concentrated in discrete compartments at the periphery of the parasite. Detailed sequence and structural analyses of these and the other P-type ATPases of P. falciparum described previously, reveals that they comprise an unusual family in several respects. Firstly, the large number of non-homologous genes so far characterised reflects the complexities of ionic regulation in the diverse environments encountered by the parasite. Secondly, the plasmodial P-type ATPase family may be classified both at primary sequence and structural levels into two distinct groups-those typical of P-type ATPases (including PfATPase4) and those which are much more divergent. A third complexity is illustrated by the fact that one of the other members [1] here termed PfATPase6, has an even greater similarity to the sarcoplasmic reticulum Ca2+ ATPases than does PfATPase4, which raises questions about the possible functional relationship between these two members.
- L31 ANSWER 7 OF 17 MEDLINE on STN
- AN 95309711 MEDLINE

- TI Cloning of a new cation ATPase from Plasmodium falciparum: conservation of critical amino acids involved in calcium binding in mammalian organellar Ca(2+)-ATPases.
- AU Trottein F; Thompson J; Cowman A F
- SO GENE, (1995 May 26) 158 (1) 133-7. Journal code: 7706761. ISSN: 0378-1119.
- AB In order to study molecules that may be involved in pH gradient formation in Plasmodium, we have identified a novel cation-translocating ATPase (P-type ATPase) gene from P. falciparum (Pf). We report the full-length nucleotide and deduced amino acid (aa) sequences of this gene that we called PfATPase4. The PfATPase4 protein shares features with the different members of eukaryotic P-type ATPases, such as a similar transmembrane (TM) organization and aa identity in functionally important regions. Interestingly, the PfATPase4 protein possesses conserved aa involved in calcium binding in mammalian organellar Ca(2+)-ATPases.
- L31 ANSWER 8 OF 17 MEDLINE on STN
- AN 95154293 MEDLINE
- TI Molecular cloning and sequence of two novel P-type adenosinetriphosphatases from Plasmodium falciparum.
- AU Trottein F; Cowman A F
- SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (1995 Jan 15) 227 (1-2) 214-25. Journal code: 0107600. ISSN: 0014-2956.
- AB We have identified two novel P-type ATPase genes from Plasmodium falciparum and report the full-length nucleotide and derived amino acid sequence of the ATPase2 gene from P. falciparum (PfATPase2). PfATPase2 is phylogenetically remote from the different members of prokaryotic and mammalian P-type ATPases but shares features with a putative membrane-spanning Ca2+ ATPase involved in ribosome function in yeast. PfATPase2 is expressed during the intraerythrocytic life cycle of the parasite and appears to be required in the late stages of its asexual development. We also present the partial sequence of another malarial gene displaying sequence similarity with the family of P-type transporting ATPases (PfATPase4). We have analysed the organisation of the genes encoding the P-type ATPases of P. falciparum and show that they are a highly dispersed gene family.
- L31 ANSWER 9 OF 17 MEDLINE on STN
- AN 95021518 MEDLINE
- TI Cloning and characterization of the vacuolar ATPase B subunit from Plasmodium falciparum.
- AU Karcz S R; Herrmann V R; Trottein F; Cowman A F
- SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1994 May) 65 (1) 123-33. Journal code: 8006324. ISSN: 0166-6851.
- The transvacuolar pH gradient determines, to a significant extent, the distribution of the antimalarial drug chloroquine in Plasmodium falciparum. A proton pump, similar to the vacuolar ATPase found in many cell types, appears to regulate a pH gradient across the membranes of acidic compartments of the parasite. In order to understand and define the components involved in the maintenance of the vacuolar pH gradient, we have cloned and characterized a gene, designated VAP B, encoding a P. falciparum homologue of the B subunit of the vacuolar ATPase. The VAP B gene encodes a protein of 494 amino acids which has between 69% and 74% amino acid identity with the sequences of vacuolar ATPase B subunits of other organisms. The VAP B gene exists as a single copy gene on chromosome 4 that gives rise to a RNA transcript of 2.4 kb. Antibodies raised to the

VAP B protein react specifically with a protein of 56-kDa, consistent with the size predicted from the gene sequence and with the homologous protein from other organisms. The 56-kDa protein is expressed throughout the asexual life cycle and subcellular localization by indirect immunofluorescence shows that the protein has a heterogeneous distribution over most of the parasite. This suggests that the function of the vacuolar proton ATPase is not confined to the regulation of the pH of the digestive vacuole.

- L31 ANSWER 10 OF 17 MEDLINE on STN
- AN 94131050 MEDLINE
- TI Plasmodium falciparum: further characterization of putative cation ATPases.
- AU Krishna S; Cowan G M; Robson K J; Meade J C
- SO EXPERIMENTAL PARASITOLOGY, (1994 Feb) 78 (1) 113-7. Journal code: 0370713. ISSN: 0014-4894.
- L31 ANSWER 11 OF 17 MEDLINE on STN
- AN 93241225 MEDLINE
- TI Cloning and characterization of a vacuolar ATPase A subunit homologue from Plasmodium falciparum.
- AU Karcz S R; Herrmann V R; Cowman A F
- SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1993 Apr) 58 (2) 333-44. Journal code: 8006324. ISSN: 0166-6851.
- The distribution of the antimalarial drug chloroquine is determined AB to a significant extent by a transvacuolar pH gradient in Plasmodium falciparum. A proton pump similar to the vacuolar ATPase found in many cell types has been suggested to maintain a pH gradient across the membranes of acidic compartments in the parasite. In order to understand and define the components involved in the mechanism of acidification of parasite vesicles, we have cloned and characterized a gene, designated VAP-A, encoding a P. falciparum homologue of the catalytic A subunit of the vacuolar ATPase. The VAP-A gene encodes a polypeptide of 611 amino acids which shows between 56 to 61% amino acid identity over its entire length with the sequences of vacuolar ATPase A subunits from several species. The VAP-A gene exists as a single copy gene on P. falciparum chromosome 13 and gives rise to a transcript of 3.7 kb. Antibodies raised against a VAP-A gene segment expressed in Escherichia coli react specifically with a 67-kDa polypeptide, consistent with the size predicted from the sequence and with the size of the corresponding polypeptide in other organisms. The 67-kDa protein is present throughout the asexual erythrocytic cycle and is expressed at similar levels in 5 P. falciparum isolates of differing chloroquine sensitivity. Sequence analysis of the coding region of the VAP-A gene from 2 chloroquine-sensitive and 3 chloroquine-resistant isolates has shown no changes that are linked to chloroquine resistance. Therefore, a proposed chloroquine resistance-linked vacuolar acidification defect does not involve mutations in the VAP-A gene in the isolates we have studied.
- L31 ANSWER 12 OF 17 MEDLINE on STN
- AN 93132070 MEDLINE
- TI A family of cation ATPase-like molecules from Plasmodium falciparum.
- AU Krishna S; Cowan G; Meade J C; Wells R A; Stringer J R; Robson K J
- SO JOURNAL OF CELL BIOLOGY, (1993 Jan) 120 (2) 385-98. Journal code: 0375356. ISSN: 0021-9525.
- AB We report the nucleotide and derived amino acid sequence of the

ATPase 1 gene from Plasmodium falciparum. The amino acid sequence shares homology with the family of "P"-type cation translocating ATPases in conserved regions important for nucleotide binding, conformational change, or phosphorylation. The gene, which is present on chromosome 5, has a product longer than any other reported for a P-type ATPase. Interstrain analysis from 12 parasite isolates by the polymerase chain reaction reveals that a 330-bp nucleotide sequence encoding three cytoplasmic regions conserved in cation ATPases (regions a-c) is of constant length. By contrast, another 360-bp sequence which is one of four regions we refer to as "inserts" contains arrays of tandem repeats which show length variation between different parasite isolates. Polymorphism results from differences in the number and types of repeat motif contained in this insert. Inserts are divergent in sequence from other P-type ATPases and share features in common with many malarial antigens. Studies using RNA from the erythrocytic stages of the malarial life cycle suggest that ATPase 1 (including the sequence which encodes tandem repeats) is expressed at the large ring stage of development. Immunolocalization has identified ATPase 1 to be in the region of the parasite plasma membrane and pigment body. These findings suggest a possible model for the genesis of malarial antigens.

- L31 ANSWER 13 OF 17 MEDLINE on STN
- AN 92134363 MEDLINE
- TI Energy dependence of chloroquine accumulation and chloroquine efflux in Plasmodium falciparum.
- AU Krogstad D J; Gluzman I Y; Herwaldt B L; Schlesinger P H; Wellems T E
- SO BIOCHEMICAL PHARMACOLOGY, (1992 Jan 9) 43 (1) 57-62. Journal code: 0101032. ISSN: 0006-2952.
- Chloroquine inhibits the growth of susceptible malaria parasites at AB low (nanomolar) concentrations because of an energy-requiring drug-concentrating mechanism in the parasite secondary lysosome (food vacuole) which is dependent on the acidification of that vesicle. Chloroquine resistance results from another energy-requiring process: efflux of chloroquine from the resistant parasite with a half-time of 2 min. Chloroquine efflux is inhibited reversibly by the removal of metabolizable substrate (glucose); it is also reduced by the ATPase inhibitor vanadate. These results suggest that chloroquine efflux is an energy-requiring process dependent on the generation and hydrolysis of ATP. Chloroquine efflux cannot be explained by differences in drug accumulation between chloroquine-susceptible and -resistant parasites because the 40-50-fold difference in initial efflux rates between -susceptible and -resistant parasites is unchanged when both parasites contain the same amount of chloroquine. Although chloroquine efflux is phenotypically similar to the efflux of anticancer drugs from multidrug-resistant (mdr) mammalian cells, it is not linked to either of the mdr-like genes of the parasite.
- L31 ANSWER 14 OF 17 MEDLINE on STN
- AN 91101662 MEDLINE
- TI Accumulation of chloroquine by membrane preparations from Plasmodium falciparum.
- AU Herwaldt B L; Schlesinger P H; Krogstad D J
- SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1990 Sep-Oct) 42 (2) 257-67
  - Journal code: 8006324. ISSN: 0166-6851.

- AB Chloroquine susceptibility and resistance have been associated respectively with the uptake and efflux of chloroquine by Plasmodium falciparum. We made membrane preparations from parasitized and unparasitized red cells in order to study chloroquine accumulation in a cell-free system. The accumulation of [3H]chloroquine by these preparations is inhibited by unlabeled chloroquine and thus is specific. Only membranes from parasitized red cells demonstrate time-dependent chloroquine accumulation; membranes from unparasitized red cells do not. Chloroquine accumulation is eliminated by detergent (0.05% Triton X-100) and reduced by a hypertonic medium, consistent with accumulation inside membrane vesicles rather than binding to membranes. Accumulation is energy dependent; it has a specific requirement for ATP, which cannot be replaced with GTP, CTP, UTP, TTP or ADP, an apparent Km of 21 microM and an apparent Vmax of 4.6 pmol (mg protein)-1 h-1. Vesicle acidification is MgATP dependent, and is reversed by NH4Cl. Chloroquine accumulation is inhibited by reduced medium pH, N-ethylmaleimide or oligomycin, but not by vanadate or ouabain. These studies demonstrate that membrane vesicles prepared from parasitized red cells provide a model system for the study of chloroquine accumulation by P. falciparum.
- L31 ANSWER 15 OF 17 MEDLINE on STN
- AN 91077466 MEDLINE
- TI Ion metabolism in malaria-infected erythrocytes.
- AU Tanabe K
- SO BLOOD CELLS, (1990) 16 (2-3) 437-49. Ref: 61 Journal code: 7513567. ISSN: 0340-4684.
- AΒ Malaria parasites of the genus Plasmodium spend much of their asexual life cycle inside the erythrocytes of their vertebrate Parasites presumably have to exploit metabolic and transport. mechanisms to adapt themselves to the host erythrocyte's physicochemical environment. This review surveys the metabolism and transport of Ca2+, alkali cations, and H+ in malaria-infected erythrocytes. The Ca2+ content of Plasmodium-infected erythrocytes increases as the parasite matures. An increase in the influx of extracellular Ca2+ into infected erythrocytes is evident at later stages of parasite development. In infected erythrocytes, Ca2+ is almost exclusively localized in the parasite compartment and changes but little in the cytosol of the host cell. The importance of Ca2+ in supporting the growth of intraerythrocytic parasites and the invasion of erythrocytes by the merozoite has been assessed by depletion of extracellular Ca2+ with chelators, or by disturbance of the metabolism and transport of Ca2+ with a variety of Ca2+ modulators. Membranes of malaria-infected erythrocytes change their permeability to alkali cations. Hence, levels of K+ decrease and levels of Na+ increase in the cytosol of infected erythrocytes. Intraerythrocytic parasites maintain a high K+, low Na+ state, suggesting a mechanism for transporting K+ inward and Na+ outward against concentration gradients of the alkali cations across the parasite plasma membrane and/or the parasitophorous vacuole membrane (PVM). Concomitantly, P. falciparum can grow in Na(+)-enriched human erythrocytes. Experimental evidence suggests that Plasmodium possesses in its plasma membrane a proton pump which is very sensitive to orthovanadate, carbonylcyanide m-chlorophenylhydrazone, a protonophore, and dicyclohexylcarbodiimide, an inhibitor of H(+)-ATPase, but is only slightly sensitive to inhibitors of bacterial and mitochondrial respiration, such as antimycin A, CN-,

or N3-, and ouabain, a Na+, K(+)-ATPase inhibitor. By operating this proton pump, parasites extrude H+ and thus generate an electrochemical gradient of protons (an internal negative membrane potential and a concentration gradient of protons) across the parasite plasma membrane. The electrochemical gradient apparently drives inward movement of Ca2+ and, possibly, glucose from the cytosol of infected erythrocytes. Little is known about the transport properties of the PVM. Recent sequence studies suggest that Plasmodium contains a cation-transporting ATPase which exhibits a high homology to the Ca2(+)-ATPase of rabbit skeletal muscle sarcoplasmic reticulum. (ABSTRACT TRUNCATED AT 250 WORDS)

- L31 ANSWER 16 OF 17 MEDLINE on STN
- AN 89040035 MEDLINE
- TI Purification of Plasmodium falciparum digestive vacuoles and partial characterization of the vacuolar membrane ATPase.
- AU Choi I; Mego J L
- SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1988 Oct) 31 (1) 71-8. Journal code: 8006324. ISSN: 0166-6851.
- AΒ Plasmodium falciparum digestive vacuoles containing ferric oxide granules were purified from parasite homogenates by centrifugation on discontinuous sucrose gradients. Digestive vacuole membranes prepared by osmotic lysis and washed with KCl showed no detectable contamination by erythrocyte membrane proteins and only minimal contamination by non-vacuolar parasite proteins. Purified vacuolar membranes were 2.6-fold enriched in total parasite membrane ATPase activity. This ATPase was optimally active at pH 7 in the presence of at least 2 mM Mg2+. Ca2+ and Mn2+ were approximately 80-90% as effective as Mg2+, and Zn2+, Co2+ and Fe2+ also exerted some stimulatory effect. The vacuolar membrane also hydrolyzed GTP, UTP, CTP and ADP, but AMP and 3',5'-cyclic AMP were hydrolyzed only one-tenth as effectively as ATP. The ATPase was unaffected by vanadate, ouabain or oligomycin but was significantly inhibited by the proton pump inhibitors NEM and NBD-Cl. Of 6 antimalarial drugs tested, quinine and quinacrine were the most effective inhibitors and mefloquine was the least effective.
- L31 ANSWER 17 OF 17 MEDLINE on STN
- AN 74085067 MEDLINE
- TI Bongkrekic acid and the adenosinetriphosphate requirement of malaria parasites.
- AU Trager W
- SO EXPERIMENTAL PARASITOLOGY, (1973 Dec) 34 (3) 412-6. Journal code: 0370713. ISSN: 0014-4894.

FILE 'HCAPLUS' ENTERED AT 14:45:35 ON 07 OCT 2003

- L32 8 SEA FILE=HCAPLUS ABB=ON PLU=ON (PLASMODIUM OR FALCIPARU
  M) AND ADENOSINETRIPHOSPHATASE
- USEA FILE=HCAPLUS ABB=ON PLU=ON L32 AND (MICROTUB? OR MICRO TUBUL? OR ((PROTEIN OR PEPTIDE OR POLYPROTEIN OR POLYPEPTIDE) AND STIMUL?))

(FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 14:47:45 ON 07 OCT 2003)

- L34 1 S L33
- L35 0 S L34 NOT L15

FILE 'HOME' ENTERED AT 14:50:06 ON 07 OCT 2003

Searcher: Shears 308-4994

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(FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
       JICST-EPLUS, JAPIO' ENTERED AT 14:40:14 ON 07 OCT 2003)
                131 S "SAKOWICZ R"?/AU
L17
                                                                            Author (s)
                561 S "BERAUD C"?/AU
L18
             10837 S "GUO J"?/AU
L19
L20
               4357 S "FREEDMAN R"?/AU
                   3 S L17 AND L18 AND L19 AND L20
L21
L22
                 42 S L17 AND (L18 OR L19 OR L20)
                108 S L18 AND (L19 OR L20)
L23
                   6 S L19 AND L20
L24
             15730 S L17 OR L18 OR L19 OR L20
L25
                 14 S (PLASMODIUM OR FALCIPARUM) AND (L22 OR L23 OR L25)
L26
                 18 S L21 OR L24 OR L26
L27
                 10 DUP REM L27 (8 DUPLICATES REMOVED)
L28
L28 ANSWER 1 OF 10 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 1
ACCESSION NUMBER:
                                 2003:454460 HCAPLUS
                                 139:31820
DOCUMENT NUMBER:
                                 Plasmodium falciparum
TITLE:
                                 kinesin motor protein KinI-1 with
                                 microtubule-stimulated ATPase activity and uses
                                 for diagnosis and treatment of malaria
INVENTOR(S):
                                 Sakowicz, Roman; Beraud,
                                 Christophe; Guo, Jun;
                                 Freedman, Richard
                                 Cytokinetics, Inc., USA
PATENT ASSIGNEE(S):
                                 PCT Int. Appl., 68 pp.
SOURCE:
                                 CODEN: PIXXD2
DOCUMENT TYPE:
                                 Patent
                                 English
LANGUAGE:
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
      PATENT NO.
                             KIND DATE
                                                         APPLICATION NO.
                                     -----
                             A2
                                     20030612
                                                         WO 2002-US38360 20021127
      WO 2003048320
            W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
           W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

2003104496

A1 20030605

US 2001-6780

20011130
                                     20030605
                                                          US 2001-6780
                                                                                 20011130
      US 2003104496
                            A1
                                                                            A2 20011130
PRIORITY APPLN. INFO.:
                                                      US 2001-6780
                                                                           A2 20020228
                                                      US 2002-86935
      The present invention relates to protein and cDNA sequences of a new
       kinesin motor protein, P. falciparum KinI-1 (PfKinI-1),
      and the use of these compns. for the diagnosis, treatment, or
      prevention of malaria. The invention provides isolated nucleic acid
      and amino acid sequences of kinesin superfamily motor protein
      KinI-1, which has microtubule stimulated ATPase activity and/or
```

antibodies to PfKinI-1, methods of screening for PfKinI-1 modulators

depolymerizes microtubules. The invention further relates to

using biol. active PfKinI-1, and kits for screening for PfKinI-1 modulators.

L28 ANSWER 2 OF 10 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER:

2003:435206 HCAPLUS

DOCUMENT NUMBER:

139:909

TITLE:

Sequences of Plasmodium

falciparum kinesin KinI-1 and use for

treating malaria

INVENTOR(S):

Sakowicz, Roman; Beraud, Christophe; Guo, Jun;

Freedman, Richard

PATENT ASSIGNEE(S):

Cytokinetics, Inc., USA

SOURCE:

U.S. Pat. Appl. Publ., 32 pp.

CODEN: USXXCO

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

I	PATENT NO.					KIND DATE			A	PPLI	CATI	ои ис	O. DATE				
-		2003104496 2003048320										780 8383	20011130				
<b>,</b>	vo	W: AE, AG, CN, CO, GE, GH,		AL,	AM,	AT,	AU,	AZ,	BA,	BB,	BG,	BR,	BY,	BZ,	CA,		
				GM,	HR,	HU,	ID,	IL,	IN,	IS,	JP,	KE,	KG,	KP,	KR,	KZ,	
			NO,	ΝZ,	OM,	PH,	LT, PL,	PT,	RO,	RU,	sc,	SD,	SE,	SG,	SI,	SK,	SL,
			•	•	•	•	TT, KG,	•	•	•	•••		VC,	VN,	YU,	ZA,	ZM,
		RW:	_	-		•	MW, DE,	•	•	•	•	•	•	•	•		
			MC,	NL,	PT,	SE,	SK,	TR,	BF,	•	•		•		•		
PRIORI	GW, ML, IORITY APPLN. INFO.					NE,	NE, SN, TD, TG			US 2001-6780				A2 20011130			
								1	US 2002-86935					A2 20020228			

AB The invention provides sequences of Plasmodium falciparum kinesin KinI-1. The invention also relates to the use of KinI-1 for the diagnosis, treatment, or prevention of malaria.

L28 ANSWER 3 OF 10 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-492112 [46] WPIDS

CROSS REFERENCE:

2002-352124 [38]; 2003-491700 [46]

DOC. NO. CPI:

C2003-131606

TITLE:

New human microtubule motor protein (kinesin motor protein KinI-3) and nucleic acid, useful for diagnosing, preventing or treating e.g. cancer,

restenosis, inflammation, neurological disorders or

disorders of vesicular transport.

DERWENT CLASS:

B04 D16

INVENTOR(S):

BERAUD, C; DAVIES, K A; FREEDMAN, R;

GUO, J; PATEL, U A

PATENT ASSIGNEE(S):

(CYTO-N) CYTOKINETICS

COUNTRY COUNT:

PATENT INFORMATION:

Searcher : Shears 308-4994

PATENT NO KIND DATE WEEK LA PG US 2003036075 A1 20030220 (200346)\*

#### APPLICATION DETAILS:

PATENT NO KIN	D	APPLICATION	DATE
US 2003036075 A	1 CIP of Div ex	US 2000-675227 US 2001-967908 US 2002-159151	20000929 20010928 20020531

#### FILING DETAILS:

PATENT NO	KIND	PATENT NO
US 20030360	75 Al CIP of	US 6461855

PRIORITY APPLN. INFO: US 2001-967908 20010928; US 2000-675227 20000929; US 2002-159151 20020531

ΑN 2003-492112 [46] WPIDS

2002-352124 [38]; 2003-491700 [46] US2003036075 A UPAB: 20030719 CR

AΒ

NOVELTY - An isolated microtubule motor protein, which has greater than 70 % sequence identity to a 1368 amino acid sequence (P1), given in the specification as measured using a sequence comparison algorithm, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) an isolated nucleic acid sequence:
- (a) encoding the microtubule motor protein described above, where the motor the protein's activity includes microtubule depolymerization activity; or
- (b) comprising a sequence which has greater than 60 % sequence identity with nucleotide comprising 6409 base pairs (N1), given in the specification;
- (2) an expression vector comprising the nucleic acid encoding the microtubule motor protein;
  - (3) a host cell transfected with the vector of (2);
  - (4) screening for modulators of KinI-3 comprising:
  - (a) providing the biologically active KinI-3;
- (b) contacting the biologically active KinI-3 with a candidate agent in a test and control concentration; and
- (c) assaying for the level of KinI-3 activity, where the KinI-3 activity consists of binding activity or ATPase activity, and where a change in activity between the test and control concentration indicates a modulator; and
- (5) a compound that modulates KinI-3, which is identified using the method of (4).

ACTIVITY - Cytostatic; Vasotropic; Immunomodulator; Antiinflammatory; Vulnerary; Antirheumatic; Antiarthritic; Antiarteriosclerotic; Antigout; Antipsoriatic; Antidiabetic; Ophthalmological; Immunosuppressive; Neuroprotective.

No biological data is given.

MECHANISM OF ACTION - ATPase Modulator; Microtubule Motor Protein Modulator.

USE - The KinI-3 protein, nucleic acid, or its modulator, is useful for diagnosing, preventing or treating cellular proliferation

> Searcher : Shears 308-4994

(e.g. cancers (e.g. bronchogenic, carcinoma, Kaposi's sarcoma, lymphoma, leukemia, osteoid osteoma, glioblastoma, etc.), hyperplasia, restenosis, cardiac hypertrophy, immune disorders or inflammation), neurological disorders, or disorders of vesicular transport. These disorders also include atherosclerosis, hemangiomas, acoustic neuromas, vascular malfunctions, abnormal wound healing, rheumatoid arthritis, Bechet's disease, gout, psoriasis, diabetic retinopathy, corneal graft rejection, glaucoma, Osler Webber syndrome, etc. The protein, nucleic acid or the KinI-3 modulator regulates cell cycle, as well as cellular proliferation. The KinI-3 protein or nucleic acid is also useful for screening therapeutic agents or KinI-3 modulators, which may be used for treating the above-mentioned diseases or disorders.

Dwg.0/9

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L28 ANSWER 4 OF 10 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 2
```

ACCESSION NUMBER: 2002:256423 HCAPLUS

DOCUMENT NUMBER: 136:274347

TITLE: Human kinesin motor protein KinI-3, protein and

cDNA sequences and tissue expression

INVENTOR(S):
Beraud, Christophe; Guo, Jun;

Freedman, Richard; Patel, Umesh A.;

Davies, Katherine A.

PATENT ASSIGNEE(S): SOURCE:

Cytokinetics, Inc., USA PCT Int. Appl., 68 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PAT	PATENT NO.				KIND DATE				APPLICATION NO. DA							
							WO 2001-US30750					20010928				
WO	W:	AE, CN, GE, LC, NO, TR, KZ,	AG, CO, GH, LK, NZ, TT, MD,	AL, CR, GM, LR, PH, TZ, RU,	AM, CU, HR, LS, PL, UA, TJ,	AT, CZ, HU, LT, PT, UG,	AU, DE, ID, LU, RO, US,	DK, IL, LV, RU, UZ,	DM, IN, MA, SD, VN,	DZ, IS, MD, SE, YU,	EC, JP, MG, SG, ZA,	EE, KE, MK, SI, ZW,	ES, KG, MN, SK, AM,	FI, KP, MW, SL, AZ,	GB, KR, MX, TJ, BY,	GD, KZ, MZ, TM, KG,
		TR,				FI, CG,	•		•	•				•		
US US	64618 6432 6436 1330	855 659 686		B:	1 1	2002 2002	0813 0820		U U	S 20 S 20	00-7: 00-7:	2451 2321	0 6	2000: 2000:	1127 1127	
PRIORITY		PT, LN.	ÌIE, INFO	SI,	LT,		FI,	RO,	MK, US 2 WO 2	CY, 000-	AL, 6752: US30	TR 27 750	A W	2000 2001	0929 0928	MC,

AB The invention provides isolated nucleic acid and amino acid sequences for human kinesin KinI-3. The invention also relates to antibodies to KinI-3. The invention also relates to methods of screening for KinI-3 modulators using biol. active KinI-3, and kits

## 10/006780

for screening for KinI-3 modulators. The invention shows that kinesin KinI-3 is unregulated in lung, colon and breast cancers.

L28 ANSWER 5 OF 10 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 3

ACCESSION NUMBER:

2002:351338 HCAPLUS

DOCUMENT NUMBER:

137:74991

TITLE:

SOURCE:

A mechanism for microtubule depolymerization by

KinI kinesins

AUTHOR(S):

Moores, Carolyn A.; Yu, Ming; Guo, Jun

; Beraud, Christophe; Sakowicz,

Roman; Milligan, Ronald A.

CORPORATE SOURCE:

Department of Cell Biology, CB227, The Scripps

Research Institute, La Jolla, CA, 92037, USA

Molecular Cell (2002), 9(4), 903-909 CODEN: MOCEFL; ISSN: 1097-2765

PUBLISHER: DOCUMENT TYPE: LANGUAGE:

Cell Press Journal English

Whereas most kinesins motor along microtubules, KinI kinesins are microtubule depolymg. machines. Surprisingly, we found that a KinI fragment consisting of only the motor core is capable of ATP-dependent depolymn. The motor binds along microtubules in all nucleotide states, but in the presence of AMPPNP, microtubule depolymn. also occurs. Structural characterization of the products of AMPPNP-induced destabilization revealed a snapshot of the disassembly machine in action as it precisely deformed a tubulin dimer. While conventional kinesins use the energy of ATP binding to execute a "power-stroke," KinIs use it to bend the underlying protofilament. Thus, the relatively small class-specific

differences within the KinI motor core modulate a fundamentally conserved mode of interaction with microtubules to produce a unique depolymg. activity.

REFERENCE COUNT:

THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 6 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER:

2003:156397 BIOSIS

DOCUMENT NUMBER:

PREV200300156397

29

TITLE:

Interaction of a KinI motor core with microtubules.

AUTHOR(S):

Moores, C. A. (1); Hekmat-Nejad, M.; Yu, M.;

Sakowicz, R.; Milligan, R. A. (1)

CORPORATE SOURCE:

(1) Dept. of Cell Biology, Scripps Research

SOURCE:

Institute, La Jolla, CA, USA USA Molecular Biology of the Cell, (Nov. 2002, 2002) Vol.

13, No. Supplement, pp. 280a. print.
Meeting Info.: 42nd Annual Meeting of the American Society for Cell Biology San Francisco, CA, USA December 14-18, 2002 American Society for Cell

Biology

÷.

. ISSN: 1059-1524.

DOCUMENT TYPE: LANGUAGE:

Conference English

L28 ANSWER 7 OF 10 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

ACCESSION NUMBER: 2002:563016 SCISEARCH

THE GENUINE ARTICLE: 570RY

Searcher : Shears 308-4994

## 10/006780

TITLE: Potential long-term toxicity of repeated orally

administered doses of artemether in rats.

Xiao S H; Yang Y Q; You Q Q; Utzinger J; Guo H F; Jiao P Y; Mei J Y; Guo J; Bergquist R; AUTHOR:

Tanner M (Reprint)

CORPORATE SOURCE: Swiss Trop Inst, POB, CH-4002 Basel, Switzerland

(Reprint); Swiss Trop Inst, CH-4002 Basel,

Switzerland; Chinese Acad Prevent Med, Inst Parasit Dis, Shanghai 200025, Peoples R China; Princeton Univ, Off Populat Res, Princeton, NJ 08544 USA; WHO, WHO Special Programme Res & Training Trop Dis, World

Bank, UNDP, CH-1211 Geneva 27, Switzerland

COUNTRY OF AUTHOR: Switzerland; Peoples R China; USA

SOURCE:

AMERICAN JOURNAL OF TROPICAL MEDICINE AND HYGIENE,

(JAN 2002) Vol. 66, No. 1, pp. 30-34. Publisher: AMER SOC TROP MED & HYGIENE, 8000 WESTPARK DR, STE 130, MCLEAN, VA 22101 USA.

ISSN: 0002-9637. Article; Journal

DOCUMENT TYPE: LANGUAGE:

English

29

REFERENCE COUNT:

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Artemether, an efficacious antimalarial drug, effectively ΔR prevents patent schistosome infections and morbidity, as established in laboratory models and in clinical trials. In view of concern about the potential long-term toxicity, rats were treated orally with 80 mg/kg artemether once every 2 weeks for 5 months. After the final treatment, routine blood test results were normal except for reversible reductions of reticulocyte counts and reversible increases in hemoglobin levels. Liver and kidney function and histopathological examination showed no differences between treated and untreated rats. Administration of 400 mg/kg artemether resulted in transient focal vesicle degeneration of the liver or slight damage to the proprius layer lamina of intestinal villi. No damage to the central nervous system tissues, including cerebrum, cerebellum, midbrain, thalamus, pons, medulla oblongata, and spinal cord, was seen at either concentration. There were no alterations in electrocardiograms during the 6-month treatment period. We conclude that 80 mg/kg artemether administered once every 2 weeks is safe, and doses of 400 mg/kg do not result in evidence of neurotoxicology.

L28 ANSWER 8 OF 10 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN 2000:878709 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: 374GN

TITLE:

A statistical-based approach to assessing the fidelity of combinatorial libraries encoded with electrophoric molecular tags. Development and

application of tag decode-assisted single bead LC/MS

analysis

AUTHOR: Dolle R E (Reprint); Guo J; OBrien L; Jin.

Y; Piznik M; Bowman K J; Li W N; Egan W J; Cavallaro C L; Roughton A L; Zhao Q; Reader J C; Orlowski M;

JacobSamuel B; Carroll C D

CORPORATE SOURCE:

PHARMACOPEIA INC, DEPT CHEM, POB 5350, PRINCETON, NJ 08543 (Reprint); PHARMACOPEIA INC, DEPT ANALYT CHEM, PRINCETON, NJ 08543; PHARMACOPEIA INC, DEPT BIOL, PRINCETON, NJ 08543; PHARMACOPEIA INC, CTR INFORMAT

& DRUG DISCOVERY, PRINCETON, NJ 08543

Searcher : Shears 308-4994

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## 10/006780

COUNTRY OF AUTHOR:

JOURNAL OF COMBINATORIAL CHEMISTRY, (NOV-DEC 2000) SOURCE:

Vol. 2, No. 6, pp. 716-731.

Publisher: AMER CHEMICAL SOC, 1155 16TH ST, NW,

WASHINGTON, DC 20036.

ISSN: 1520-4766.

Article; Journal DOCUMENT TYPE:

FILE SEGMENT: PHYS; LIFE LANGUAGE: English

REFERENCE COUNT: 78

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB A statistical sampling protocol is described to assess the fidelity of libraries encoded with molecular tags. The methodology, termed library QA, is based on the combined application of tag decode analysis and single bead LC/MS. The physical existence of library compounds eluted from beads is established by comparing the molecular weight predicted by tag decode with empirical measurement. The goal of sampling is to provide information on overall library fidelity and an indication of the performance of individual library synthons. The minimal sampling size n for library QA is 10x the largest synthon set. Data are reported as proportion (p) +/- lower and upper boundary (1b-ub) computed at the 95% confidence level (alpha = 0.05). As a practical demonstration, library QA was performed on a 25 200-member library of statine amides (size = 40 x $63 \times 10$ ). Sampling was conducted three times at n similar to 630beads per run for a total of 1902 beads. The overall proportions found for the three runs were consistent with one another: p =84.4%, 1b-ub = 81.5-87.2%; p = 83.1%, 1b-ub = 80.2-85.95; and p = 81.5-87.2% 84.5%, 1b-ub = 81.8-87.3%, suggesting the true value of p is close to 84% compound confirmation. The performance pi of individual synthons was also computed. Corroboration of QA data with biological screening results obtained from assaying the library against cathepsin D and plasmepsin II is discussed.

L28 ANSWER 9 OF 10 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 4

1998:630381 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 129:331033

TITLE: Identification of potent inhibitors of

Plasmodium falciparum

plasmepsin II from an encoded statine

combinatorial library

AUTHOR(S):

Carroll, Carolyn Dilanni; Patel, Hitesh; Johnson, Theodore O.; Guo, Tao; Orlowski, Marc;

He, Zhen-Min; Cavallaro, Cullen L.; Guo, Joan; Oksman, Anna; Gluzman, Ilya Y.; Connelly, James; Chelsky, Daniel; Goldberg,

Daniel E.; Dolle, Roland E.

Department Biology, Pharmacopeia, Inc., CORPORATE SOURCE:

Princeton, NJ, 08540, USA

SOURCE: Bioorganic & Medicinal Chemistry Letters (1998),

8(17), 2315-2320 CODEN: BMCLE8; ISSN: 0960-894X

Elsevier Science Ltd. PUBLISHER:

Journal DOCUMENT TYPE: LANGUAGE: English

GI

Searcher : Shears 308-4994

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$$\mathbb{R}^{4} \xrightarrow[H]{0} \mathbb{R}^{3} \xrightarrow[N]{0} \mathbb{N} \xrightarrow[H]{0} \mathbb{N}^{1}$$

An encoded 13,020-member combinatorial library I [R1 = Me, Bu, MeO(CH2)3, Ph(CH2)4, PhCH2, 2-pyridylmethyl, 3-pyridylmethyl; R2 = CH2Ph, Me, CH2CHMe2; R3 = side chain from 31 natural and unnatural L- and D-amino acids; R4 = Ph, 2-naphthylmethyl, 2,4-(MeO)2C6H3, cyclopropyl, 2-carboxy-4-methylcyclohexyl, 4-(4-HOC6H4)C6H4, 5-phenyl-2-pyrrolylethyl, Me3C, 4-methylcyclohexyl, 2-naphthyloxymethyl, Et2NCH2CH2, 4-(Me2NCH2)C6H4, n-heptyl, 3-tetrahydrofuryl, 4-[(HO2C)2CH0]C6H4, HOCHMeCH2, 2,4-Cl2C6H4O(CH2)3, PhCH2] was synthesized containing a statine core. Evaluation of this library with plasmepsin II, an aspartyl protease required for Hb metabolism in the malaria parasite, led to the identification of potent and selective inhibitors as well as novel structure-activity relationships.

Ι

REFERENCE COUNT:

18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 10 OF 10 MEDLINE ON STN

ACCESSION NUMBER: 93338845 MEDLINE

DOCUMENT NUMBER: 93338845 PubMed ID: 1307277

TITLE: Effect of sodium artesunate on Plasmodium

yoelii analysed by flow cytometry.

AUTHOR: Han W S; Zhou W Q; Wang B X; Li Z M; Zuo L F;

Guo J W

CORPORATE SOURCE: Department of Parasitology, Hebei Medical College,

Shijiazhuang.

SOURCE: CHUNG-KUO CHI SHENG CHUNG HSUEH YU CHI SHENG CHUNG

PING TSA CHIH CHINESE JOURNAL OF PARASITOLOGY AND

PARASITIC DISEASES, (1992) 10 (3) 204-7. Journal code: 8709992. ISSN: 1000-7423.

PUB. COUNTRY: China

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: Chinese

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199309

ENTRY DATE: Entered STN: 19930917

Last Updated on STN: 19930917 Entered Medline: 19930902

AB The effect of sodium artesunate on Plasmodium yoelii-infected mouse erythrocytes was analysed by flow cytometry. The results showed that malarial DNA content in experimental group was obviously decreased 2-5 hours after the drug was administered, fluorescence distribution of malarial DNA almost disappeared within 24 hours after the administration. Thus we deem that sodium artesunate can inhibit the DNA synthesis in P. yoelii.

FILE 'HOME' ENTERED AT 14:43:32 ON 07 OCT 2003

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Result
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Q9lus1 arabidopsis	Q9LUS1	10	799	11.5	89.	45
Q9avp4 nicotiana t	Q9AVP4	10	703		790.5	44
Q8iis9 plasmodium	6SI18Ö	ហ	3334	11.6	791	43
ש	Q8IHY4		2849		793.5	42
Q940y8 arabidopsis	Q940Y8		684	11.6	794	41
	Q8ICZ4		1437	٠	795	40
Q8iei5 plasmodium	Q8IEI5		1192	11.6	795.5	9
l arabid	Q9LW81		706		795.5	38
w1 oryza sat	Q94GW1	10	800	11.6	796	37
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	Q814X5	U	1605	11.7	798	5
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	808I8Q	ഗ	2206	11.8	804	28
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Q8i5x5 plasmodium .	Q815X5	υı	2612	11.8	808	26
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Q8t2m5 dictyosteli	Q8T2M5	U	2472		810.5	24
_	Q8IDR0	ហ	3848	11.9	813	23
Q8iau8 plasmodium	QBIAU8	ຫ	1774		815.5	22
Q8ibk6 plasmodium	Q8IBK6	υī	2041	11.9	816	21
œ	Q8IHV8	ហ	7	11.9	817.5	20
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Q8iiq7 plasmodium	Q811Q7	ഗ	1483		19.	18
Q8t806 dictyosteli	Q8T806	ທ	901	12.0	824	17

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SEQUENCE '1351 AA; 156007 MW; 8B69594BFD73C788 CRC64;	EMBL; AE014851; AAN36517.1;	Nature 419:498-511(2002).	falciparum.";	"Genome sequence of the human malaria parasite Plasmodium	Fraser C.M., Barrell B.;	Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,	McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,	Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,	Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,	Chan MS., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,	Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,	Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,	Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,	MEDLINE=22255705; PubMed=12368864;	STRAIN=3D7;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=36329;	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	Plasmodium falciparum (isolate 3D7).	PFL2165W.	Kinesin-like protein, putative.	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	01-MAR-2003 (TrEMBLrel. 23, Created)	Q8I4YO;	Q814Y0 PRELIMINARY; PRT; 1351 AA.	0 0 1 1	RESULT 1	

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Query Match Best Local Sim Matches 1288;

Similarity

100.0%; Score 6842; DB<sub>3</sub>5; 100.0%; Pred. No. 7.1e-268; tive 0; Mismatches 0;

Length 1351;

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Submitted (SEP-2002) to the E EMBL; AL844507; CAD51342.1; -
Hypothetical protein.
SEQUENCE 2577 AA; 299292 M
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NCBI_TaxID=36329;
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194 MIDGVLLRKIGVNSQNDBSSRSHAILNIDLKDINKNTSLGKIAFIDLA 241	183 TNYYQSFIKNDNIPYINQTNIFDNNIKNKYMLDDK 217	144 ISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILRVLTKEELILK 193	23 LILYPSLMPYVECIIEKIKKIKNENITFFPAIEQFNFSIEHAVSSYQTGTQTFNNHPNFY 18	LNIYDKDNTKGIF 14	52 RHEFIVDKVFDDTVDNFTVYENTIKPLIIDLYENGCYCSCFAYGQTGSGK 101	5 IQEKLQEKKKKKKKKMSDRKEDKNDIILNKNEEEDNINNNNIILYKSFDDFKINYSYKTK 6	3	Query Match 12.8%; Score 876.5; DB 5; Length 3207; Best Local Similarity 23.3%; Pred. No. 1.7e-27; Matches 388; Conservative 245; Mismatches 520; Indels 513; Gaps 76;	hetical protein. NCE 3207 AA; 377920	ature 419: MBL: AE014	man malaria par	ngs L.M., Subramanian G.M., Mungal D.J., Hoffman S.L., Newbold C., D	gut J., Hart D., Mather M.W., Valoya A. H., Fraunholz M.J., Roos D.S., Ralph S.	J.A., KULHELLOIG K., SMILDERY S.L., CIAIR A., NYES S., S.S., Nene V., Shallom S.J., Sub B., Petterson J., William V., Shallom S.J., Sub B., Petterson J., William V., William	arther M.O., Hair M., Fully E., Wille O., Bertillain M., A) arthen J.M., Pain A., Nelson K.E., Bowman S., Paulsen I arther T	22255705; PubMed=12368864;	ENCE	ID=36329;	im falciparum (isolate 3D7). Le Blyeolata: Boicompleya: Haemosporida	cal protein.	01-MAR-2003 (TremBirel. 23, Last sequence update) 01-MAR-2003 (TremBirel. 23, Last annotation update)	003 (TremBLrel. 23, Created)	LT 3 Q0 Q0 PRELIMINARY; PRT; 3207 AA. Q81HQ0:	1859 × 1859	1270 K 1270	1804CSDKNYKLNNCINKSMDLKYSTNNIIINMMNNNIFPNECNNKYVCGSDDNMFLNK 1858	EYQNKSANSVLLNVS	1751 QKVDEMDKAGHMNKVDFINSGNNDYKNKLDIINNKMYDQFNNVNTGRYHSSNI 1803	1194MCHICNNNPDDQFHFYAYSRLEKDIINLIMLRQ 1226	1691 TIFTNSRSTEPKŚLSENSDVTNAKDEINVIGLANSISTGNSTGNSTECVKDGNKDLIGYI 1750	1164 VILTKLLLLFKKNVDTQINNETSDLRKDLV 1193	:

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Hypothetical protein.
MALGP1.307.
Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 3248 AA;
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Q8IB09;
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Pred. No. 9.3e-27;
3; Mismatches 438;
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Frasser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                              QBILC9;
                                                                                                                                                                                                                                         Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                       Hypothetical PF14 0315.
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CG5792 protein. 6/101.

Dictyostelium discoideum (

Eukaryota; Mycetozoa; Dict
Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A "Sequence and Analysis of Chromosome 2 of Dictyostelium.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AC116965; AAM33216.1; -.

InterPro; IPR002110; ANK.
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
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Eukaryota; Alveolata;
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01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 1681 AA;
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Best Local Sin
Matches 332;
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M. Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Knights A., Konfortov B., Kyes S., Lawke N., Lawson D., Lennard N.,
A Hine A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
A Line A., Maddison M., Kelean J., Mooney P., Moule S., Murphy L.,
A Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch B.,
A Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch B.,
A Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Secuence of Plasmodium falciparum chromosomes 1 3-9 and 13 ".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulston J.E., Craig A., Newbold C., Barrell B.C "Sequence of Plasmodium falciparum chromosomes Nature 419:527-531(2002).
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Hall N., Pain A.,
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Eukaryota; Alveolata;
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Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 5.4e-26;
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                                                                                                                                                                                                                                                               SQIIGMKKNDVIYSDMSMNYENMNNINNYNINNSNNHNDLL----PNNINDQYN----
                                                                                                                                                                                                                                                                                                            AQSIYEKRKVLLTKLLLLFKKNVDTQINN---ETSDLRKDLVMCHICNNNPDDQFHFYAY
                                                                                                                                                                                                                                                                                                                                                              ----VNHS-NSMKSIGEYNMNNYNLHNIRMS--KGDDNNTNKVDVGNHVNN-----
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EMBL, ACI17082, AMM34352.1; -.

InterPro; IPR003034; SAP.

Fram; PP02037; SAP, 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDKNYLID-LNNKEQKDKNIHGCDNN-----IIQNRNDFEKKKKTN--FYNNNNIVIVN
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                                                                                                                                                                                                                                                                                                  ----HNIKNFNNNEYL-------SYFQKNVDTI--INNCLNSLDIS--
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                                                                                                                                                                                                           SMYDDTKEILNNILLSKYKAEKDNVIKK----YINEDIKN-----MSLEEI
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M Hall N., Pain A., Berriman M., Churcher C., Harris D., Hall N., Pain A., Berriman M., Churcher C., Barron A., Brooks K., A Mungall K., Bownan S., Atkin R., Baker S., Barron A., Brooks K., A Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Chark L., Clark R., Corton C., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Chillingworth T., Christodoulou Z., Clark L., Clark R., Doggett J., A Chillingworth T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lemard N., A Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lemard N., A Chine A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L., A Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E., A Cliver K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Seger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., A Seger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Sulston J.E., Craig A., Newbold C., Barrell B.G;

"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";

"Nature Alg. 527-531 (2002)
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Q81350;
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Eukaryota; Alveolata;
NCBI_TaxID=36329;
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TRHYKDSSNEYNK----YNGNDNICNDHNLSHTLSKYDNFVLSDNNNDNSNNYSLKEEN
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  DVDFHNIKNFNNNEYLSYFQK----NVDTIINNCLNSLDISSMYDDTKEILNNILLSKYK 1128
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Hypothetical protein, expressed.
MAL6P1 48.
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EMBL; AL844505; CAD50319.1; -.
Hypothetical protein.
SEQUENCE 2874 AA; 334409 MW; 65541406B59DBDCB CRC64;
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Eukaryota; Alveolata;
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23.6%; Pred. No. 1.1e-25;
tive 213; Mismatches 412;
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EMBL; AE014847; AAN36303.1;
Hypothetical protein.
SEQUENCE 2432 AA; 284064
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01-JUN-2002 (TrEMBLrel. 21, Creat.
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01-MAR-2003 (TrEMBLrel. 23, Last.
Hypothetical 102.9 kDa protein.
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Best Local Similarity 26.5%;
Matches 278; Conservative 13
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Gloeckner G., Bichinger L., April J.F., Guigo R., Kumpf K. Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K. Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel "Supence and Analysis of Chromosome 2 of Dictyostelium.";
Supmitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC115682; AAL92689.1; --
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PROSITE; PS00039; DEAD ATP_HELICASE; 1.

Hypothetical protein.

SEQUENCE 901 AA; 102858 MW; C3B6954
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       1125
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Pred. No. 6.8e-26
9; Mismatches 28
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Qy       337 KSTCINEEDDTNTERISILDSKGSEMNAS	Qy 223 LKDINKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRA 276	Query Match Best Local Similarity 25.5%; Pred. No. 1.6e-25; Matches 319; Conservative 160; Mismatches 333; Indels 439; Gaps 57;  Qy 189 ELILKMIDGYLLRKIGVNSQN	Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmo falciparum."; Nature 419:498-511(2002). EMBL; AE014837; AAN35697.1; SEQUENCE 1483 AA; 173923 MW; F93DB19A2A34D5F1 CRC	Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Ky Chan MS., Nene V., Shallom S.J., Shh B., Peterson J. Pertea M., Allen J., Selengut J., Haft D., Mather M.W. Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S McFadden G.I., Cummings L.M., Subramanian G.M., Mungall Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., D.	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBI_TaxID=36329; [1] SEQUENCE FROM N.A. STRAIN=3D7; MEDLINE=22255705; PubMed=12368864; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,	JIIQ7  LMAR-2003 (TrEMBLrel  LMAR-2003 (TREM	CY	720 GSKKCDHLECSEIILKNEFTKHIKKLHHHHK 1172 LFKK
RESULT 19  QBILS4 ID QBILS4; PRELIMINARY; PRT; 4466 AA. AC QBILS4; DT 01-MAR-2003 (TrEMBLrel. 23, Created) DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) DE Hypothetical protein. GN PF14_0170. OS Plasmodium falciparum (isolate 3D7).	OY 1094 NVDTTINNCLNSLDISSMYDDTKEILNNILLSKYKAEKONVIKKYINEDIKNNSLE 1149  1094 INDITINNCLNSLDISSMYDDTKEILNNILLSKYKAEKONVIKKYINEDIKNNSLE 1149  1095 INNTIDNNNNNKDITSTNLKSTLLQTKTKRRVKKKTTDETENNNVENNEA 1035  OY 1150EIDKTAQSIYEKRKVULTKLLLLFKKNVDT 1179  OY 1150	1030 NNVDNNKKRVDNNVDNNVD	Db 750 KKNVDHNNNTPYQKKELNIIKKDDKVNIKNIIMKNIKREDNNTAPYNSGVNLSS 804  Qy 1004 NEDIYNKEMEGKHIRLDDQDKYDDND 1029	910 -EMKDNHIKSNNNNSSSSSSSNNNIYNN-INDDDTFQNDYCHND	QY         790         KNTSNIQNINTNKNNQDGNVNYSMNPCHYNI.NDKNYLIDLNNKEQKDKNIHGCDNNIIQN         849               .   .   .   .   .   .   .   .   .	Qy         673 NSINNSNMNSINNSNMNSNSIYKSNYNSNQSISDVQIRYVNEMDTSNKANDNIFFDA 729	429 630 481	Db 268 NIYNNYNGNNNNSNNNNNSSNNNHMSNNNNNNNNNNNNNNNNNNNN

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Matches 399;
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Cardner M.J., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
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Hypothetical protein.
SEQUENCE 4466 AA; 519821
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MEDLINE=22255705;
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NCBI_TaxID=36329;
[1]
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                             GSKLTMFSYDPQKNKDNTFFKSNINKMEDNTPKDILYESRNVSNMNGNVLLGLNKNTHHD
                                                        AMDSDKNHIPFRDS-----ELTKVLRDIFVGKS-KSIMIANISPTISCCEQTLNTLRYSS
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llarity 21.9%;
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53; Mismatches 505
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Best Local Similarity
Matches 318; Conserv
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Seeger K., Murphy L., Harris
Quail M., Barrell B.;
Submitted (SEP-2002) to the E
EMBL; AL844507; CAD5.262.1; -
Hypothetical protein.
SEQUENCE 1774 AA; 200169 M
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                         EYQNKSANSVLLNVSSN-----NGDIILLNKKLVQDNIKNSMDH---
                                                                                                         DTSNPQKMKLNNFPF
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Plasmodium falciparum Eukaryota; Alveolata; NCBI\_TaxID=36329; (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. PRELIMINARY; protein. Apicomplexa; Harris (isolate 3D7). 23, Created)
Last sequence
Last annotation EMBL/GenBank/DDBJ ŋ., PRT; sequence update)
annotation update) Berriman Haemosporida; 1774 ₿ <u>;</u> Pain databases Plasmodium

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CRC64

Hall

Score 815.5; DB 5 Pred. No. 2.8e-25; 9; Mismatches 411

DB 5;

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Qy  428 KIKKNKKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1429 DDISICSNEDVNDIIYNINRTDDILKRLMYLSNNYYNNMIEYDNYILHSYQHNDHILNEL  345 DDINTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNNKI  1489 NNNTVTYYNNIKKKKNFNNQLLPRTKRNEDFIFNNHIVTENNIYNNNNNNKLADSEIM  387NRGKINDKIERNNILKNKSFDKPREGFTSTFGKYSSLNDID  387	Qy 180 KILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFID 239  :	Hypothetical protein.  Hypothetical protein.  SEQUENCE 3848 AA; 454964 MW; 57D2700BEA3F5A9A CRC64;  SEQUENCE 3848 AA; 454964 MW; 57D2700BEA3F5A9A CRC64;  Sequence of the sequ	EPP en en en en en en en en en en en en en	RESULT 23  Q8IDR0 PRELIMINARY; PRT; 3848 AA.  AC Q8IDR0; (TrEMBLrel. 23, Created)  DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  DE Hypothetical protein.	Qy 1088 LSYFQKNVDŤIINNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVIKKYINEDIKNMS 1147  Db 1574IINIKVHNNISNSLFSNNMSNYNVVSENVNINNNS 1609  Qy 1148 LEEIDKTAQSIYEKRKVLLTKLLLLFKKNVDTQINNETSDLRK 1190

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DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation up
DE Hypothetical 278.5 kDa protein.
DE Dictyostelium discoideum (Slime mold).
S Dictyostelium discoideum (Slime mold).
Pukaryota; Mycetozoa; Dictyosteliida; Dictyos
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noege
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC115593; AAL92295.1; -.

Hypothetical protein.

SEQUENCE 2472 AA; 278497 MW; 30CCF7157D4008A7 CRC64;
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Pred. No. 6e-25;
Nismatches 40
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Noegel A.A.;
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MEDLINE=99376085; PubMed=10448855;

MEDLINE=99376085; PubMed=10448855;

Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,

Churcher C.M., Craig A., Davies R.M, Devlin K., Feltwell T.,

Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby

Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,

Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,

Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,

Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;

Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
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Nature 400:532-538(1999).
EMBL; AL034559; CAB39023.1;
HSSP; P33176; 1BG2.
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01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
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01-MAY-1999
                                                       InterPro; IPR001451; Hexapep_transf.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00132; hexapep; 4.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
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Eukaryota; Alveolata;
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PROSITE; PS00411; KINESIN MOTOR DOMAIN1; PS50067; KINESIN MOTOR DOMAIN2;
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153KLYDLTQKKGWAALENGKKEVVVKDLKILRVLTKE 188	105 MLGSQPYGQSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFISFYBIYCG 152 	51 ERHEFIVDKVFDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYT 104   :  ::::::       :        :	NSKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDM 	Query Match 11.8%; Score 808; DB 5; Length 2612; Best Local Similarity 24.2%; Pred. No. 8e-25; Matches 373; Conservative 220; Mismatches 434; Indels 514; Gaps 78;	Nature 419:498-511(2002).  NATURE 419:498-511(2002).  HMBL; AED14845; AAN36159.1;  HYDOTHETICAL PROTECTION.  SEQUENCE 2612 AA; 311421 MW; C950B6E466E3D1C5 CRC64;	Carucci D.J., Hoffman S.L., Newboll Barrell B.; nce of the human malaria parasite	om S.J., igut J., Hagut J., Ha	NE=22255705; PubMed=1 er M.J., Hall N., Fun on J.M., Pain A., Nel	36329;	1 protein. 1 protein. 1 protein. 1 protein. 1 protein. 1 protein. 1 protein. 1 protein. 1 protein. 1 protein. 1 protein. 1 protein.	OBISES OBISES OBISES OBINAR-2003 (TremBLrel. 23, Created) O1-MAR-2003 (TremBLrel. 23, Last sequence update) O1-MAR-2003 (TremBLrel. 23 Last sequence)	26	:  : : :  :   :  :  :  : -FQENIKHEHKDEVSLYVKKKKIKKKM	1138 YINEDIKNMSLEEIDKTAQSIYEKRKVLLTKL 1169	1088 LSYFQKNVDTIINNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVIKK 1137 	1028 NDNNNVDNNKKNNVDNNVDNNVDNNVDNNDKNNVDNNDDDDDDDD	968 IYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDD 1027	KNVAKMLLKGNLNTANFILDDDTIKNMNSN
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Qy 457 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Qy 313 PTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSKGSE 361	CY 156 DLICKERWYARLENGKESVYKULKI IR YDTKEELILKMIDGVLLRKIGVISOND 210 21 EVIQTKSVQLRLQKEKEEGNIKMEKFKKRKRQISDKED	Query Match 11.8%; Score 807; DB 5; Length 1918; Best Local Similarity 21.1%; Pred: No. 6.6e-25; Matches 361; Conservative 204; Mismatches 468; Indels 674; Gaps	OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  OX NCBI TaxID=44689;  RN [1]  RP SEQUENCE FROM N.A.  RC STRAIN=AX4;  RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,  RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,  RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;  RA Tunggal B., Cox E., Quail M.A., Platzer M. Rosenthal A., Noegel A.A.;  RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";  Sequence (MAR-2002) to the EMBL/GenBank/DDBJ databases.  EMBL, AC115586; AAL92259.1; -  SQ SEQUENCE 1918 AA; 217043 MW; BFBA078455C60D8E CRC64;	RESULT 27  Q8SSW3  ID Q8SSW3  AC Q8SSW3;  DT 01-JUN-2002 (TrEMBLrel. 21, Created)  DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  DT 01-CCT-2002 (TrEMBLrel. 22, Last annotation update)  DT 01-CCT-2002 (TrEMBLrel. 22, Last annotation update)  DE Erythrocyte membrane protein PFEMP3.  OS Dictyostelium discoideum (Slime mold).	Qy       988 TILLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNAVDNNAVDNNAVDN 1047         1       : : :         : :         : :         : :   :           : : :                   : : : :
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Qy 537 556  Db 856 TDINENKYNDIKSSNTKNNDQQNKNVNKHNNNNKLIHITTLENNNKVVTLKEGQHIHIS 915  Qy 557 RDNIKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDN 603	QY       439 NYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Db 562 HIEEDIKEHIIDK	Qy 168 ENGKKEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKD 225	RN [1]  RP SEQUENCE FROM N.A.  RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,  RA Quail M., Barrell B.;  RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  SQ EMBL; AL844506; CAD50900.1;  KW Hypothetical protein.  SQ SEQUENCE 2206 AA; 258401 MW; D4ED711AE470383C CRC64;  SQ SEQUENCE 2206 AA; 258401 MW; D4ED711AE470383C CRC64;  SQ Ouery Match  11.8%; Score 804; DB 5; Length 2206;  Best Local Similarity 22.7%; Pred. No. 9.9e-25;  Matches 353; Conservative 226; Mismatches 381; Indels 598; Gaps 73;	RESULT 28  QRIBUB QRIBUB ID QBIBUB PRELIMINARY; PRT; 2206 AA.  AC QRIBUB; DT 01-MAR-2003 (TrEMBLrel 23, Created) DT 01-MAR-2003 (TrEMBLrel 23, Last sequence update) DT 01-MAR-2003 (TrEMBLrel 23, Last annotation update) DE Hypothetical protein. GN PF07_0061. GN PF07_0061. OS Plasmodium falciparum (isolate 3D7). OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. OX NCBI TaxID=36329;	
RESULT 29 Q811894 ID Q81894 AC Q81894; AC Q81894; DT 01-MAR-2003 (TrEMBLrel. 23, Created)	GRILTRS FLVVEYQ   :EDK NIHKK 12         EIEKK 18	1111MYDDTKEILNNILLSKYKAEKDNVI	Db 1419 NNILNIDKNISNVNSPIKMENVGENISTCQHINNINYMVN	OY 830 NNKEQKOXHGCDNALIQN		. ·

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Plasmodium falciparum (isolate 3D7).

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

MCBI_TaxID=36329;
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L., Barrell B.;
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Pred. No. 3.5e-24;
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Best Local (
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                         Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S. Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B. Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A. McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q815Z0;
                                                                                                                                                                                                         EMBL; AE014844; AAN36144.1;
Hypothetical protein.
SEQUENCE 1785 AA; 204851
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Eukaryota; Alveolata;
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                                                                                                                                                                                                                                                                     Nature 419:498-511(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22255705; PubMed=12368864;
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annotation update)
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	1172 LFKKUVDTQINNETSDLRKDLVMCHICNNNPDDQEHFYAYSRLEKDIINLIMLRQI 1227	1116 KEILNNIILLSKYKAEKDNVIKKYINEDIKNMSLEBIDKTAQSIYEKRKVLLTKLLL 1171	1063DNNNYDNDDDDVDFHNIKNFNNNEYLS-YFQKNVDTIINNCLNSLDISSMYDDT 1115	1013 EGKHIRLDDQDKYDDNDNNNVDNNVDNNVDNNVDNNVDNNDKNNV 1062	954 -FTIRKWNTNINSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEM 1012 .	901 MKNNEMKDNEMKDNHIKSNNNNSSSSSSSNNNIYNNINDDDTFQNDYCHNDNT 953 	843 DNNIIQNRNDFEKKKKTNFYNNNNIVIVNNNMGNNNSPRMKYGLCGSHTSIDNMKNNB 900   :: :  :	789 NKNTSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLNNKEQKDKNIHGC 842	748NNNNNNNNNNNNNDVENYNNRDGTNNSMKLYAYNSHNLFQPDN 788	699NSNQSISDVQIRYVNEMDTSNKNINDNIFFDAISCDNIMYPNITININNINN 747	641 KNTHHDISTKDENHNDNKINNGVINIINNSNVNSINNSNMNSINNSNMNSNSIYKSNY 698	589 KLTMFSYDPQKNKDNTFFKSNINKM-EDNTPKDILYESRNVSNMNGNVLLGLN 640	529 TSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSSCDNIMNKKKNNLHLARHSVGS 588	477 NDSSSMVNNMINH-MINNNINNNINVNNNNNNNNN-NNNSHNNHLPQPNYAFTD 528	417 FGKYSSLNDIDKIKKNKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	357 SKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPREGFTST 416	297 DIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILD 356	237 FIDLAGSERGADTVSQNKQFQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLR 296 879RDTSTLGTFLKIKPFSNPIPLPIGSIFK 906	:  
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                                                           Plasmodium falciparum (isolate 3D7)
Eukaryota; Alveolata; Apicomplexa;
                                                                                                              PFI0225W.
                                                                                                                             Hypothetical protein.
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                                                             Apicomplexa; Haemosporida; Plasmodium.
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Last annotation updat
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RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Arkin R., Baker S., Barron A., Brooks K.,
RA Mungall K., Bowman S., Arkin R., Baker S., Barron A., Brooks K.,
RA Mungall K., Bowman S., Arkin R., Grilliangworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davis R., Davis P., Dear P., Dearden F., Doggett J.,
RA Cronin A., Davis R., Davis P., Dear P., Dearden F., Doggett J.,
RA Cronin A., Davis R., Davis P., Dear P., Dearden F., Doggett J.,
RA Cronin A., Davis R., James K.D., Johnson D., Kerhornou A.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Humphray S., Jagels R., James K.D., Johnson D., Lennard N.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Cliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
RA Aller A., Rutherford K.M., Sanders M., Simmonds M.,
Segger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
"Sequence of plasmodium falciparum chromosomes 1, 3-9 and 13.";
RM Murphy R., Marchical B.G;
"Sequence of plasmodium falciparum chromosomes 1, 3-9 and 13.";
RM Hypotherical T., Schill T., Schill R., Marchical B.G;
"Mulli, Al,929355, CAD51731.1; -.
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Matches 363;
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                              NILISNDENFSSDSSNMYNIINAKHNDKLNTQKLFLLENDKICANSHISSNMNQTEYISL
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                                                                                   VDNNENVDSNENVDN-NENMDRNDNMYNNEN-VDNSKMFINCNKSQRSNIKKSNSTNSTR
                                                                                                            IERN-NILKNKSFDKPREGFTSTFGKYSSLNDIDKIK-----
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Apicomplexa; Haemosporida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 419:498-511(2002).
EMBL; AE014843; AAN36060.1;
Hypothetical protein.
SEQUENCE 2940 AA; 348040
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NCBI_TaxID=36329;
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                                            VNYSMNFCHYNLINDKNYLIDLINNKEQK-----DKNIH-----GCDNNIIQNRNDF
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                    -DMC---VNNDEICGD-NGKTQKGVNRKVGPGRKKNVNFKMEENADTNVNYEKINI
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	18 EKKKKDSDI	Query Match 11.7%; Score 798; DB 5; Length 1605; Best Local Similarity 22.4%; Pred. No. 1.3e-24; Matches 384; Conservative 222; Mismatches 455; Indels 652; Gaps 75;	Nature 419:498-511(2002).  EMBL; AE014851; AAN36522.1;  Hypothetical protein.  SEQUENCE 1605 AA; 188160 MW; CBDB7FA9E1D7C268 CRC64;	Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium falciparum.";	Chan MS., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G. T. Chumings I. M. Subramanian G.M. Mungall C.	MEDLINE-2255705; PubMed=12368864; MEDLINE-2255705; PubMed=12368864; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen I.B. Butherford K. Callabert S. Craid A. Kyen S.	NCBI_TaxID=36329; [1] SEQUENCE FROM N.A. STRAIN=3D7.	protein. alciparum (isolate 3D7). lveolata: Apicomplexa: Haemospoj	23, Created) 23, Last sequence 23, Last annotati	INT 35 . ORITHINARY. DRT. 1605 AA.	1237 LYQFLVVEYQNKSANSVLLNVSSNNGDIILLNKKLVQDNIKNSMDH-NNI 1285 	1179 TQINNETSDLRKDLVMCHICNNNPDDQFHFYAYSRLEKDIINLIMLRQIWCESENLRL 1236	1119 LNNILLSKYKAEKDNVIKKYINEDIKNMSLEEIDKTAQSIYEKRKVLLTKLLLLFKKNVD 1178  :       :  :	1068 DNDDDDVDFHNIKNFNNNEYLSYFQKNVDTIINNCLNSLDISSMYDDTKEI 1118	1014 GKHIRLDDQDKYDDNDNNNVDNNVKNNVDNNVDNNNVDNNVDNNDKNNVDNNVV 1067     : :	970 QNDDIIYTINSLNDYMSNTLLHFKEKYTY-PTLSTNEDIYNKEME 1013  :   :   :      :    :  :  :           1081 NNNQMDYTVTDYSSGNSAILIDKQNCETDYLENVQYNHTPNISLNGLTYN 1130	914 NHIKSNNNNNSSSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNIY 969  :   :   :	854 EKKKKTNFYNNNNIVIVNNNMGNNNSPRMKYGLCGSHTSIDNMKUNEMKUNEMKDNEMKD 913 
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815 FCHYNLNDK-NYLIDLNNKEQKDKNIHGCDNNIIQNRNDFEKKKKTNFYNNN 865	NNKISFKSIKNMNIVKKYLKKDDVNKNKNTKSILNINHKDDNK		672 VNSINNSNYMSINNSNYMSNSIYKSNYNSNQSISDVQIRYVNEMDTSNK 720	EGVHYLNVDDNNNDD	. 596DPQKNKDNTFFKSNINKMEDNTPKDILYESRNVSNMNGNVLIGLNKNTH 644	575 KKNNL	552IMNK 574 553	YLNETASTI KFAQRAKMVK	INVNNNNNN-NNNNNNSHNNH	405 SFDKPREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYNDNTINKKHNNNNNNNNNN 464	345 DDTNTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKUK 404 	285 PFRDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEE 344	232 -LGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHI 284   ::          :  :  :  :  :  :  :  :  :	174 VVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTS 231	123 AAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKE 173    ;:  ;       ;:  ;       ;:	112	78 LIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPY	54

399;

Gaps

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RESULT

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    Query Match
Best Local
                                                                                                                                            MEDLINE=2255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman.R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
"Genome sequence of the human malaria parasite Plasmodium
"selenger""
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF14_0363.
Plasmodium falciparum
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01-MAR-2003
                                                                                                          Nature
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                                                               AAN36976.1;
AA; 226572
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24.6%;
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Score 797.5; DB 5;
Pred. No. 1.6e-24;
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                                      GNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSSSSSSSNNNIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --YSSRVKNFKNKSTCIN--EEDDTNTERISILDSKGS--EMNASSIENVVIKSNHLLSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ---NDENNIIKHNVNONNNEVI-VMNNOTEEQINDNKFIKPLNNITGIDPKKKNIYNTV
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                                                                                                                              -NDFEK--
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                                                                                                                              --KKKTN--
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Hsing Y.-I.C., Chow T.-Y., Wu H.-P., Chao Y.-Y.
Su C.-L., Chen C.-S., Shaw J.-F.;
"Oryza sativa PAC P0431605 genomics sequence.'
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; AC087551; AAK70904.1; -.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gramene; Q94GW1; -.
InterPro; IPR001752; kinesin_motor.
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Colled coll; Microtubules; Mot
SEQUENCE 800 AA; 88189 MW; D9B330375AC6
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                                                                                 DTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQY
                                                                                                                                                                          SKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFD
     AAGDIFTFLN--, LYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK 180
                                                  EQVSNDEVYRETVEPIIFIIFQR-TKATCFAYGQTGSGKTYTM---QP-----LPLR
                                                                                                                                                     PRELIMINARY;
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Pred. No. 8.2e
96; Mismatches
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                                                                                                                                                                                                                                                   92;
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01-OCT-2000
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopsermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
similarity to kinesin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                         features of clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Columbia; MEDLINE=20277480;
                                                                                                   PRINTS; PRO0380; KINESINHEAVY.

SMART; SM00129; KISc; 1.

SMART; SM00129; KISc; 1.

PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

ATP-binding; Coiled coil; MicroFubules; Motor protein.

SEQUENCE 706 AA; 79246 MW; 059658E9E69282F2 CRC64;
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HSSP; P17119; 3KAR.
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Pfam; PF00225; kinesin; 1.
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d (MAR-1998)
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Pred. No. 7.6e
91; Mismatches
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Query Match Query Match 11.6%; Score 795.5; DB 5; Length 1192; Best Local Similarity 25.5%; Pred. No. 1.2e-24; Matches 295; Conservative 163; Mismatches 367; Indels 332; Gaps 48;  y 327 YSSYNDKKSTCINEEDDTNTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNN 384	Plasmodium falciparum (isolate 3D7).  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  NCBI TaxID=36329;  (1)  SEQUENCE FROM N.A.  Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,  Harris B., Lennard N., Hall N., Atkin R., Chillingworth C., Doggett J.,  Ormond D., Sanders M., Hayls R., Hall S., Quail M., Barrell B.;  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  EMBL, AL844509; CAD52272.1;  SEQUENCE 1192 AA; 139166 MW; 9CEB8FDDBD0A5A46 CRC64;	IS  QBIEI5 PRELIMINARY; PRT; 1192 AA.  QBIEI5; PRELIMINARY; PRT; 1192 AA.  QBIEI5; PRELIMINARY; PRT; 1192 AA.  QBIEI5 PLASHBURE1. 23, Created)  O1-MAR-2003 (Trembure1. 23, Last sequence update)  O1-MAR-2003 (Trembure1. 23, Last annotation update)  Plasmodium falciparum asparagine-rich protein.  MALI3P1.63.		566 -GMAQERIPKETI-QMKSRDMPREDMKKSNSDDNLNALLQEEEDLVNAHRKQVED 618 448 NTINKKHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	340 CINEEDDINTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNNKIN 387	236 AFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIDFRDSELTKVL 295	3 SKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLVIDEPRYKVDMTKYIERHEFIVDKVFD 62
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PRELIMINARY; PRT; 1437 AA.  2003 (TrEMBLrel. 23, Created) 2003 (TrEMBLrel. 23, Created) 2003 (TrEMBLrel. 23, Last sequence update) 2003 (TrEMBLrel. 23, Last sequence update) 23.a liveolata; Apicomplexa; Haemosporida; Plasmodium. 23.a Alveolata; Apicomplexa; Haemosporida; Plasmodium. 23.a liveolata; Apicomplexa; Haemosporida; Plasmodium. 24.8 liveolata; Apicomplexa; Haemosporida; Plasmodium. 25.a liveolata; Apicomplexa; Haemosporida; Plasmodium. 26. FROM N. A. 27. Sanders M. Hayes R., Hall S., Opail M., Barrelli 28. Liveolata; Apicomplexa; Holmosporida; Plasmodium. 29. Sanders M., Hayes R., Hall S., Opail M., Barrelli 20. Sanders M., Hayes R., Hall S., Opail M., Barrelli 21. Liveolata; Apicomplexa; FoADA05528A741DA CRC64; 21. Liveolata; Discomplexa; FoADA05528A741DA CRC64; 22. Liveolata; Discomplexa; FoADA05528A741DA CRC64; 23. LIVEOLATIC MARKETSIGKIAFIDLAGSERGADTVSOMCOTOTDG-ANIMESLI 24. RESIDENTALISH SINGUAL FOADA05528A741DA CRC64; 24. RESIDENTALISH SINGUARY SELTKVLRDITYGKSKSIMIANISHNISH 25. LILENEKSINIKWINININININNINNINNINNINNINNINNINNINNINNI	A MUNTANDENNO ANVARIO MONTANTANTINO TO TRANSPORTANTAN AND TRANSPORTANTANTAN AND TRANSPORTANTANTAN AND TRANSPORTANTAN AND TRANSPORTANTANTAN AND TRANSPORTANTANTAN AND TRANSPORTANTANTANTANTANTANTANTANTANTANTANTANTANT	;	5 1
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PRELIMINARY; PRT; 1437 AA.	NGVINIINNSNVNSINNSNNNSINNSNNNSNSIYKSNVSNQSISDVQIR	66	.Q
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PRELIMINARY; PRT; 1437 AA.  11-MAR-2003 (TYEMBLICEL 23, Created)  1-MAR-2003 (TYEMBLICEL 23, Last sequence update)  1-MAR-2003 (Tyemblicel 23, Las	KISNEKHINKKEKNKNAGEDDEEDVTITDINVLEKEKSKNQKIKNNENQHNKKNNIGQNN 7	6	므
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NYNFFGNNCIHCKSYKNEIKN-LTLQIKLMKEEILKYKQLIMSSGINEKFEKN 1406	YQFLVVEYQNKSANSVLLNVSSNNGDIILLNKKLVQDNIKNSMDHN 1283	FLSCNSINENFDDANEYNNKINGFKGENHYSYNNVGKNISTDINESYNNSENHFNLFG	YAYSRLEKDIINLIMLRQIWCESENLRLL	SLGINSPCLTKEDFFNCAGNNNVVENKSKEYNISDNGINDSCDYTNNLLNI	ESIDKTAQSIYEKRKVLLTKLLLFKKNV-DTQINNETSDLRKD	NDCMFLFKDNLSISGLGNVNLCNEKNMINESLNNIFKGDNINNNM	NSLDISSMYDDTKEILNNILLSKYKAEKDNVIKKYINEDIKNM	1YNKK-	NINKNAUZDNNAZDNNAZDNAZDNDEKNNAZDNDZDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	MQENENMFNKNIRSNVKNILDYITMENKNMNNNNNNNNNNN	KEMEGKHIRLDDQDKYDDNDNNVD	IHEKGRDN-NSIFLETDNYNN	NSSSSSSNNNIYNNINDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQNDDIIYTINS	QLLMNHGQLDDKDNMKNNKKDDNNIAFNVLTNKENKCNNNYNNIGRAITTAVGTSSF	SPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNN	VHNKENKNNINNRINVISNNNNNINNIEEDSKNNSNDILTNLNDTNIH	VIIQNRNDFEKKKTNFYNNNNIVIVNNNMGNNN	: .: :       :  :   :   :	
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Hypothetical protein.
Dictyostelium discoideum (
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   STRAIN=AX4;
Gloeckner G., Eichinge
Lehmann R., Baumgart (
Tunggal B., Cox E., Qu
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OBT224;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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Eichinger L., Szafranski K., Pachebat J., Dear
aumgart C., Parra G., April J.F., Guigo R., Kump
ox E., Quail M.A., Platzer M., Rosenthal A., Noe
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Hypothetical protein.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Di
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Hypothetical protein.
SEQUENCE 699 AA; 79820 M
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
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Matches 18
                                                                               InterPro; IPR001410; DEAD.
InterPro; IPR00150; Helicase C.
InterPro; IPR00330; SNF2 N.
Pfam; PF00271; helicase C; 1.
Pfam; PF00271; helicase C; 1.
SMART; SM00480; HELICC; 1.
SMART; SM00490; HELICC; 1.
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01-JUN-2002
01-MAR-2003
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Q8T1J6;
01-JUN-2002
01-JUN-2002
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"Evolution of the ABC transporters of
Submitted (FEB-2002) to the EMBL/GenB.
EMBL; AF482386; AAL91492.1; -.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequ
01-OCT-2002 (TrEMBLrel. 22, Last anno-
Hypothetical 174.9 kDa protein.
Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                  Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P. Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noege "Sequence and Analysis of Chromosome 2 of Dictyostelium.", Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC116425; AAL99110.1; -. Interpro: TDR001410. npm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding.
SEQUENCE 815 AA;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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           Hypothetical SEQUENCE 19
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190; HELICc; 1.
I protein; ATP-binding; Helicase; Hydrolase.
1518 AA; 174934 MW; 8FE54FB086031500 CRC64;
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EMBL/GenBank/DDBJ databases.
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RESULT 9
Q95ZG5
ID Q95ZG5
AC Q95ZG5
DT 01-DEC-2001
DT 01-DEC-201
DT 01-MAR-2003
DE PUTATIVE RNAI
GN DRNA.
OS DICTYOSTEILU
OC EUKATYOTA; MO
OX NCBI_TAXID=4.
RN [1]
RP SEQUENCE FROM
RC STRAIN=AX4;
RA MATTENS H.;
RA MATTENS H.;
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Q8SSS8
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InterPro; IPR000719; Prot kinase.
InterPro; IPR000408; Reg_chr_condens.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00632; HECT; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF000615; RCC1; 3.
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01-JUN-2002
01-MAR-2003
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-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50237; HECT; 1.

PROSITE; PS50237; HECT; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00626; RCC1_2; 2.

PROSITE; PS00626; RCC1_3; 6.

PROSITE; PS00626; RCC1_3; 6.
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Eukaryota; Mycetozoa; Dic
                                                                    Eukaryota; Mycetozoa;
NCBI_TaxID=44689;
                                                                                      Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida;
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SEQUENCE 18
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18; Conser
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Dictyosteliida;
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Pred. No.
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3. 6.2e-08;
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                                                                                         Dictyostelium
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RESULT 11
Q9U573
ID Q9U57
AC Q9U57
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Q9NA13
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Pfam; PF00271; helicase C; 1.
Pfam; PF00636; Ribonuclease 3; 2.
Pfam; PF00176; SNP2 N; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00490; HELICC; 1.
  Q9U573;
Q9U573;
01-MAY-2000
01-OCT-2000
01-MAR-2003
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01-OCT-2000
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InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR00193; Insep_areceptor.
Pfam; PF01365; RYDR_ITPR; 2.
PRINTS; PR00779; INSPSRECEPTR.
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PROSITE; PS50142; RNASE 3_2; 2.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 2994 AA; 348080 MW;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Inositol 1,4,5-trisphosphate receptor-like protein.
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InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Ax2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=44689;
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InterPro; IPR000330; SNF2 N.
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                                                                                                                                                                                                                                                                                                                     Similarity
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  (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                              Conservative
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                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                    360526 MW;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                Score 18;
Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                    381ECEA20A7C84A2 CRC64;
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chemotaxis in
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9.5e-08;
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9e-08;
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Matches 17
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Best Local S
Matches 18
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Q8MNQ5;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                   Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P. Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf Tunggal B., Cox E., Quail M., Platzer M., Rosenthal A., Noege "Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00320; WD40; 4.

PROSITE; PS50197; BEACH; 1.

PROSITE; PS500678; WD REPEATS 1; 1.

PROSITE; PS50082; WD_REPEATS 2; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

REPEAT; WD repeat.

SEQUENCE 3619 AA; 408069 MW; 24B74A
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InterPro; IPR001680; WD40.
Pfam; PF02138; Beach; 1.
Pfam; PF00400; WD40; 5.
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Kwak E., Gerald N., Larochelle D.A.,
Maready M., De Lozanne A.;
"Lysa, a protein related to the mous
                                                                                                                                                                                Hypothetical protein. SEQUENCE 104 AA; 1
                                                                                                                                                                                                                                                                                                                                                               STRAIN=AX4;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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                                              742
      75
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                                                                                                               Similarity
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                                                                                          Conservative
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100.0%; Pr
                                                                                                                                                                              12132 MW;
                                                                                                             1.3%;
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                                                                                                               Score 17;
Pred. No.
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Pred. No.
                                                                                                                                                                                7694A678A730A5F4 CRC64;
                                                                                          Mismatches
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1.1e-07;
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                                                                                                                                    Length 104;
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                                                                                             Indels
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RESULT
Q8MP24
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01-MAR-2003 (TrEMBLrel. 2:
Hypothetical protein
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01-JUN-2002 (TrE
01-OCT-2002 (TrE
HSPC305 10/100
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                  Q8T1B5
Q8T1B5;
Q1-JUN-2002
01-JUN-2002
01-OCT-2002
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01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                  Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P. Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf Tunggal B., Cox E., Quail M., Platzer M., Rosenthal A., Noege "Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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Q9XY02;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
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Q8ST23;
01-JUN-2002 (TrE
01-JUN-2002 (TrE
01-OCT-2002 (TrE
HDCKB03P 10/100.
SEQUENCE FROM N.A. STRAIN=GI; MEDLINE=99287788; I Orii H., Kato K., U
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                                                                                             Dugesia japonica (Planarian).
Eukaryota; Metazoa; Platyhelminthes;
Paludicola; Dugesiidae; Dugesia.
MCBI TaxID=6161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kump Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noe "Sequence and Analysis of Chromosome 2 of Dictyostelium."; submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=44689;
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Eukaryota; Mycetozoa; Dic
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    Umesono Y.,
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כ R., Kumpf
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RESULT 18
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ID QBMX77
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PROSITE; PS00027; HOMEOBOX 2; 1.
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Q8MNN2;
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      Gloeckner
                                                                                                  Hypothetical protein.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dic
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Dev. Biol. 210:456-468(1999).
-i- SUBCELLULAR LOCATION: NUCLEAR EMBL; AB024409; BAA77405.1; -.
HSSP; P02833; 9ANT.
                      SEQUENCE FROM
STRAIN=AX4;
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PF11_0468.
Plasmodium falciparum (
Eukaryota; Alveolata; A
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Q8IHR1;
01-MAR-2003
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01-MAR-2003
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MEDLINE=22255705; PubMed=12368864; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
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Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K., Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., I Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL84505; CAD50400.1; -.
Hypothetical protein.
SEQUENCE 371 AA; 43460 MW; 8A81197CA8F81BC2 CRC64;
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Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., I
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC116965; AAM33218.1; -.
InterPro; IPR001159; DS_RBD.
Pfam; PF00035; dsrm; 1.
PARST; SM00358; DSRM; 1.
SMART; SM00358; DSRM; 1.
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                                                                                                                                                                     SEQUENCE
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Apicomplexa; Haemosporida;
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.,_Doggett J.,
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EMBL; AE014843; AAN36048.1;
Hypothetical protein.
SEQUENCE 384 AA; 46253 MM
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Q25768;
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McFadden G.I., Cummings L.M., Subramanian G.M., N
Venter J.C., Carucci D.J., Hoffman S.L., Newbold
Fraser C.M., Barrell B.;
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                                                                                                                                  SEQUENCE FROM N.A.
Schreiber M.G., Deutsche U.,
Submitted (DEC-1989) to the EMBL; X17489; CAA35525.1; -.
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Asparagine-rich antigen (Clone
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Schreiber M.G., Deutsche U.,
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Asparagine-rich antigen (Clone 14Cl) (Fragment).
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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oold C., Davis N
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01-JUN-2002 (TEMBLrel. 21, Last
01-CT-2002 (TEMBLrel. 22, Last
01-CT-2002 (TEMBLrel. 22, Last
Hypothetical 49.6 KDa protein.
Dictyostelium discoideum (Slime
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STRAIN=AX4;
Gloeckner G., Eichinger L.,
Baumgart C., Pa.
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Pfam; PF01529; zf_DHHC; 1.
PROSITE; PS0216; ZF_DHHC; 1.
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Dictyostelium discoideum (Slime mold).
                                                                                                                       Hypothetical SEQUENCE 43
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426 AA; 48
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llarity 100.0%; Pred. No. 1.
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Best Local :
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01-OCT-2002
01-OCT-2002
01-MAR-2003
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Eukaryota; Metazoa; Plat
Paludicola; Dugesiidae;
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                                                                                                                                                                                                                                                                                                    Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases EMBL; AB091062; BAC10918.1; -. InterPro; IPR001766; TF Fork head.
Pfam; PF00250; Fork head; 1.
                                                                                                                                                                                                                                          ProDom;
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EMBL; AE014851; AAN36532.1; -.
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Eukaryota; Alveolata;
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Apicomplexa; Haemosporida; Plasmodium
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Best Local Similarity Matches 17; Conserv
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              Gloeckner G., Eichinger L., Szafranski K., Pachebat J., De Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., K. Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., "Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC115685; AAL92706.1; -... InterPro; IPR000504; RNA rec_mot.

PROSITE; PS50102; RRM; 1.
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"Sequence and Analysis of Chromosome 2 of Dictyostellum.";
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Pfam; PR02582; DUF155; 1.
Hypothetical protein.
SEQUENCE 511 AA; 58641 MW
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Eukaryota; Mycetozoa; Dictyosteliida;
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Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., l
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC116425, AAL99099.1; -.
Hypothetical protein.
SEQUENCE 537 AA; 63290 MW; A935AD400FE8137D CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
Hypothetical 63,3 kDa protein.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyo
     Hypothetical protein.
Dictyostelium discoideum (Slime mold)
Eukaryota; Mycetozoa; Dictyosteliida;
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de HOSTOS E.L., Benhayon D., Berger M., Gu W.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
EMBL; AF051898; AAC05577.1; -.
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Dictyostelium discoid
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EMBL; AC117072; AAM33146.1; -.

Hypothetical protein.

SEQUENCE 587 AA; 66683 MW; 4B960B35F9379E06 CRC64;
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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SEQUENCE 597 AA; 68757 MW; 4FA0150
                     SEQUENCE FROM N.A
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Submitted (AUG-1996) to the EMBL; U66369; AAB06761.1; -
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SEQUENCE 608 AA; 68205 M
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                                                                  Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P. Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noege "Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC116984; AAM33199.1; -. Hypothetical protein.

SEQUENCE 616 AA; 71182 MW; 9940E42E65B85FDD CRC64;
                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Dictyostelium discoideum (Slime mold)
Eukaryota; Mycetozoa; Dictyosteliida;
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Hypothetical 71.7 kDa protein.
Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida;
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InterPro; IPR001849; PH:
InterPro; IPR000306; Znf FYVE.
InterPro; IPR000306; Znf FYVE.
Pfam; PF01363; FYVE; 1.
Pfam; PF00169; PH; 1.
SMART; SM00064; FYVE; 1.
SMART; SM00033; PH; 1.
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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EMBL; AC115581; AAL92233.1; ...

EMBL; IFR001466; Beta lactamase.
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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01-OCT-2002 (TrEMBLrel. 22,
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milarity Conserva MNSKIKVVVRK MNSKIKVVVRK MNSKIKVVVRK MNSKIKVVVRK	; FILE REFERENCE: CYTOP083; CURRENT APPLICATION NUMBER: US/10/006,780; CURRENT APPLICATION NUMBER: US/10/006,780; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2 ; LENGTH: 1288 ; TYPE: PRT ; ORGANISM: Plasmodium falciparum	Seque Seque Publi SENER APPI APPI APPI TITI	ALIGNMENTS	7 0.5 653 15 US-10-184-655-402 Sequence 402, 7 0.5 653 15 US-10-188-774-402 Sequence 402, 7 0.5 653 15 US-10-188-775-402 Sequence 402, 7 0.5 653 15 US-10-194-462-402 Sequence 402, 7 0.5 653 15 US-10-194-462-402 Sequence 402, 7 0.5 653 15 US-10-196-745-402 Sequence 402, 7 0.5 653 15 US-10-196-762-402 Sequence 402, 7 0.5 653 15 US-10-197-695-402 Sequence 402,	7 0.5 653 15 US-10-183-019-402 Sequence 402, 7 0.5 653 15 US-10-184-618-402 Sequence 402, 7 0.5 653 15 US-10-184-625-402 Sequence 402, 7 0.5 653 15 US-10-184-625-402 Sequence 402, 7 0.5 653 15 US-10-184-627-402 Sequence 402, 7 0.5 653 15 US-10-184-645-402 Sequence 402, 7 0.5 653 15 US-10-184-654-402 Sequence 402,	979 7 0.5 653 15 US-10-179-516-402 Sequence 402, App 980 7 0.5 653 15 US-10-179-519-402 Sequence 402, App 981 7 0.5 653 15 US-10-180-540-402 Sequence 402, App 982 7 0.5 653 15 US-10-180-540-402 Sequence 402, App 983 7 0.5 653 15 US-10-180-545-402 Sequence 402, App 984 7 0.5 653 15 US-10-183-006-402 Sequence 402, App 985 7 0.5 653 15 US-10-183-006-402 Sequence 402, App 986 7 0.5 653 15 US-10-183-017-402 Sequence 402, App 986 7 0.5 653 15 US-10-183-017-402 Sequence 402, App	7 0.5 653 15 US-10-179-708-402 Sequence 402, 7 0.5 653 15 US-10-176-479-402 Sequence 402, 7 0.5 653 15 US-10-176-479-402 Sequence 402, 7 0.5 653 15 US-10-176-916-402 Sequence 402, 7 0.5 653 15 US-10-176-916-402 Sequence 402, 7 0.5 653 15 US-10-179-507-402 Sequence 402,	7 0.5 653 15 US-10-194-423-402 Sequence 402, 7 0.5 653 15 US-10-195-897-402 Sequence 402, 7 0.5 653 15 US-10-195-901-402 Sequence 402, 7 0.5 653 15 US-10-195-902-402 Sequence 402, 7 0.5 653 15 US-10-196-743-402 Sequence 402,	7 0.5 653 15 US-10-188-773-402 Sequence 402, 7 0.5 653 15 US-10-188-781-402 Sequence 402, 7 0.5 653 15 US-10-194-361-402 Sequence 402,
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CURRENT APPLICATION NUMBER: US/10/006,780
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 355
TYPE: PRT
ORGANISM: P. Falciparum
US-10-006-780-6
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US-10-006-780-4
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US-10-006-780-6
                                                                                                                                           Sequence 4, Application US/10006780 Publication No. US20030104496A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 354; Conservative
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APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
APPLICANT: Graud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: NOVEL MOTOR PROTEIN OF P.
TITLE OF INVENTION: METHODS FOR ITS USE
FILE REFERENCE: CYTOPO83
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APPLICANT: Beraud, Christophe
APPLICANT: Guo, Jun
APPLICANT: Freedman, Richard
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                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10006780

Publication No. US20030104496A1

APPLICANT: Sakowicz, Roman

APPLICANT: Beraud, Christophe

APPLICANT: Beraud, Christophe

APPLICANT: Freedman, Richard

APPLICANT: Freedman, Richard

ITILE OF INVENTION: METHODS FOR ITS USE

FILE REFERENCE: CYTOP003

CURRENT APPLICATION NUMBER: US/10/006,780

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 332

TYPE: PRT

CDEANNISM: D Falcicaring
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                                               VDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYAA 124
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CURRENT APPLICATION NUMBER: US/10/006,780
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 361
TYPE: PAT
ORGANISM: P. Falciparum
US-10-006-780-8
RESULT 6
US-09-801-368-36
; Sequence 36, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
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US-10-006-780-8
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Best Local Similarity 100.0%;
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APPLICANT: Beraud, Christophe
APPLICANT: Guo, Jun
APPLICANT: Freedman, Richard
TITLE OF INVENTION: METHODS FOR ITS USE
FILE REFERENCE: CYTOP083
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                                                                                                                                                                                                                                                                                                                                                   TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA
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                                                                                                                                                                                       ERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKS
                                                                                                                                                                                                                                                 VLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGS
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                                                                                                                                                                                                                                                                                                              AGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILR 183
                                                                                                                                                                                                                                                                                                                                                                                                         SIMIANISPTISCCEQTLNTLRYSSRVKNFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMIANISPTISCCEQTLNTLRYSSRVKNFKN 336
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                                                                                                                          KSIMIANISPTISCCEQTLNTLRYSSRVKN 333
                                                                                                                                                                    ERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKS
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                                                                                                          KSIMIANISPTISCCEQTENTERYSSRVKN 331
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; Pred. No. 1.6e-298;
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 RESULT 8
US-09-994-485-8
; Sequence 8, Application US/09994485
; Patent No. US20020142429A1
; GENERAL INFORMATION:
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Best Local S
Matches 17
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Best Local :
                                                                                                                                                                      Matches
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APPLICANT: Milne, Todd
APPLICANT: NO. US20020128250Alman, Thea
APPLICANT: Solama, Sofie
APPLICANT: Salama, Sofie
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Eric
TITLE OF INVENTION: Methods for Improving Secondary
TITLE OF INVENTION: Methods for Improving Secondary
TITLE OF INVENTION: MOMBER: US/09/801,368
CURRENT APPLICATION NUMBER: US 09/487,558
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 36
LENGTH: 666
TYPE: PRI
TYPE: PRI
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TYPE: PRI
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Publication No. US20030180953A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOPTWARE: Patentin version 3.1
SEQ ID NO 7714
LENGTH: 213
TYPE: PRT
ORGANISM: Candida albicans
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                                                                                                                                                   ch 1.2%; Score 16; DB 12; 1 Similarity 100.0%; Pred. No. 1.8e-06; 16; Conservative 0; Mismatches 0;
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17; Conserv
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Holtzman, Doug
Madden, Kevin
TNNNNNNNNNNNNN 187
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Milne, Todd
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Pred. No.
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5.7e-07;
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                                                                                                                                                                                                                                     Length 213;
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RESULT 9
US-09-832-292-12
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                                                                            GENERAL INFORMATION:
APPLICANT: RYAZANOV, ALEXEY
APPLICANT: RYAZANOV, ALEXEY
TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
FILE REFERENCE: 601-1-098CIP
CURRENT FILING NUMBER: US/09/832,292
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 09/632,131
PRIOR APPLICATION NUMBER: 09/632,131
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 45
                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 732
                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09832292 Patent No. US20020177205A1
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TYPE: PRT
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ORGANISM: Dictyostelium discoideum
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
FILING DATE: <Unknown>
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 732 amino acids
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TELEPHONE: 201-487-5800
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Hait, William N.
                                                                                                                                                                                                                                                                                                                                                                                                                                    355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 601-1-078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/994,485
FILING DATE: 27-No. US20020142429A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: David A. Jackson, Esq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF SEQUENCES:
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; Pred. No. 5.3e-0
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Sequence 7565, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for CURRENT APPLICATION NUMBER: US/10/032,585

CURRENT APPLICATION NUMBER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: Patentin version 3.1

SEQ ID NO 7565

LENGTH: 798
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US-10-032-585-7565
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LENGTH: 758
TYPE: PRT
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Saccharomyces cerevisiae
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Milne, Todd
No. US20020128250Alman, 7
Royer, John
Salama, Sofie
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Silva, Jeff
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Madden, Kevin
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100.0%; Pred. No. 5.4e-06;
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Pred. No.
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TYPE: PRT

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US-09-801-368-132; Sequence 132, Application US/09801368; Patent No. US20020128250A1
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; Sequence 50, Application US/10087464
; Publication No. US20030059436A1
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Matches 16; Conserv
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LENGTH: 961
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
NUMBER OF SEQ ID NOS: 440
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                                                          APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Li, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
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               PRIOR APPLICATION NUMBER: US 06/272,930 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 59
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SOFTWARE: PatentIn version 3.0
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Similarity 100.0%;
16; Conservative (
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Silva, Jeff
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Salama, Sofie
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No. US20020128250Alman,
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Holtzman, Doug
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; SEQ ID NO 50
; LENGTH: 1331
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-464-50
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US-10-135-322-17
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Publication No.
                                                                                                                           SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10304095
Publication No. US20030134275A1
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Best Local Similarity
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APPLICANT: Love, Ruschelle A.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
FILE REFERENCE: 47714-5009-US
CURRENT APPLICATION NUMBER: US/10/304,095
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                              APPLICANT: Long, David M. APPLICANT: Metz, Anneke APPLICANT: Love, Ruschel
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PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 43
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CURRENT APPLICATION NUMBER: US/10/135,322
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                         PRIOR FILING DATE: 2002-06-14
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                                                                                                                                                             NUMBER OF SEQ ID NOS: 49
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NAME/KEY: unsure
LOCATION: (330)...(335)
OTHER INFORMATION: Xaa at position 330 = Leu or Ile;
                                                                   LENGTH: 2184
TYPE: PRT
ORGANISM: Plasmodium falciparum
                                                        FEATURE:
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16; Conserv
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KAUPPINEN, L
RIIKONEN, M
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No. US20020173017A1
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ilarity 100.0%; Pred. No.
Conservative 0; Min--
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100.0%; Pred. No.
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. 8.9e-06;
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US-10-304-095-6
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Best Local S
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LENGTH: 2690
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APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
                                                                                                                                                                                      APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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CURRENT FILING DATE: 2002-06-28
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APPLICANT: Chen, Jian
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NAME/KEY: unsure
LOCATION: 2039-2065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                     Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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No. US20030068684A1
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                                                          Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                       Desnoyers, Luc
                                                                                                                                                                                    Chen, Jian
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Goddard, Audrey
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Vo. US20030044930A1
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Pred. No.
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Pred. No.
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1.4e-05;
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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 35
; LENGTH: 2690
; TYPE: DNA
; ORGANISM: Homo Sapien
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Matches
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/632, PRIOR FILING DATE: 2000-08-03 PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2002-06-28
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Penn, Sharron G.
                                                                                                                                                                                 PRIOR
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CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 2039-2065
OTHER INFORMATION: unknown base
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NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                  APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                          FILING DATE: 2000-09-21
                                                                             FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
                                                                                                  APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
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                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00661
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100.0%; Pred. No.
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09/774,203
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; TYPE: PRT ; ORGANISM: Human US-10-422-866-2
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US-10-422-866-4
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
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SOFTWARE: Annomax Sequence Listing
SEQ ID NO 47535
LENGTH: 73
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Best Local
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/422,866
CURRENT FILING DATE: 2003-04-23
CRICK APPLICATION NUMBER: US/09/722,129
PRIOR FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/422,866
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: US/09/722,129
                                                                                                                                                                                          APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. US20030170857A1el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1054
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                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                      PRIOR FILING DATE: 2000-11-24
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 46
OTHER INFORMATION: EST_HUMAN HIT: BF327361.1, EVALUE 2.20e+00
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ORGANISM: Human
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ORGANISM: Homo sapiens
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                                                    ENGTH: 492
                                                                      ID NO 2
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100.0%; Pred. No. 2e-05;
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Pred. No.
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APPLICANT: Kennedy, Brian
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: YEAST
FILE REFERENCE: 0050.1491-005
CURRENT APPLICATION NUMBER: US/09/826,752
CURRENT FILING DATE: 20010-40-05
PRIOR APPLICATION NUMBER: US 08/396,001
PRIOR PILING DATE: 1995-02-28
PRIOR PILING DATE: 1995-02-28
PRIOR APPLICATION NUMBER: PCT/US94/09351
PRIOR FILING DATE: 1994-08-15
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR FILING DATE: 1993-08-16
PRIOR APPLICATION NUMBER: US 09/323,433
PRIOR FILING DATE: 1999-06-01
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US-09-826-752-6
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US-10-304-095-8
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CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US/09/417,485
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 8
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Best Local Similarity
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                                                                                                               SEQ ID NO 6
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Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Long, David M.
APPLICANT: Metz, Anneke M.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Guarente, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 47714-5009-US
                                            LENGTH: 888
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                    NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Application US/09826752
US20010026930A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claus, James J. Cole, Francesca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Austriaco Jr., Nicanor
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100.0%; Pred. No.
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   1.2%;
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   Score 15;
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. 3.1e-05;
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   9;
   Length 888;
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RESULT 24
US-10-032-585-7575
; Sequence 7575, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
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US-09-839-185-2
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-541-8587 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By Expression of SERK
Interacting Proteins
                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
CORRESPET: 3054 Cornwallis Road
STREET: 3054 Cornwallis Road
                                                                                                                                                                               742 NNNNNNNNNNNNN 755
                                                                                                                                                          262 NNNNNNNNNNNNN 275
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STATE: NC
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          CLONE: 3A35
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100.0%; Pred. No. 0.00021
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                                                                  Sequence 298, Application |
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
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US-09-801-368-298
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US-10-195-144-37
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APPLICANT:
APPLICANT:
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                                                        APPLICANT:
                         APPLICANT:
          APPLICANT:
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TYPE: PRT
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      Holtzman, Doug
Madden, Kevin
Maxon, Mary
                                                      Hecht, Peter
                                                                                                                      Application US/09801368
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; ORGANISM: Raphanus sativum US-10-195-144-37
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SEQ ID NO 7575
LENGTH: 458
TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/10195144 Publication No. US20030126646A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF TITLE OF INVENTION: PLANTS
FILE REFERENCE: 16313-0136
CURRENT APPLICATION NUMBER: US/10/195,144
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/305,026
PRIOR PILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/305,363
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 128
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/308,736 PRIOR FILING DATE: 2001-07-30
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
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                                                                                       Local Similarity 100.0%;
523 FAYGOTGSGKTYTM 536
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                       92 FAYGQTGSGKTYTM 105
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LANDRY, BENOIT S.
CHEUNG, WING
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                                                                        Conservative
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100.0%;
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                                                                                           Score 14; 
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                                                                          Mismatches
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                                                                                                           DB 15;
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. 0.00025;
                                                                                         0.00053;
                                                                                                         Length 1062;
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery; FILE REFERENCE: 10182-005-999; CURRENT APPLICATION NUMBER: US/10/032,585; CURRENT FILING DATE: 2001-12-20; NUMBER OF SEQ ID NOS: 8000; SOFTWARE: PatentIn version 3.1; SEQ ID NO 7237; LENGTH: 397
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US-10-032-585-7237
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                                                                                                                                                          RESULT 28
US-10-032-585-7930
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Best Local Similarity
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                                                                                                   Sequence 7930, Application US/10032585 Publication No. US20030180953A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7237, Application US/10032585
Publication No. US20030180953A1
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR PRIOR PRIOR DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PRIOR PRIOR PRIOR 10-20
NUMBER OF SEQ ID NOS: 440
                                               APPLICANT: Terry, Roemer v.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
           APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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FILE REFERENCE: 10182-005-999
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Candida albicans
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Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salama, Sofie
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US20020128250Alman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 14;
100.0%; Pred. No.
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100.0%; Pred. No. 0.
100.0%; Mismatches
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US-10-032-585-7930
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US-10-060-019-31
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                                                                                              ; Sequence 31, Applica
; Publication No. US20
; GENERAL INFORMATION:
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Matches
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 7930
LENGTH: 941
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Best Local Similarity 100.0%;
Marches 13; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 134
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-12-20
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            APPLICANT: Tyers, Mike
APPLICANT: Willems, Andrew
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.10USU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-10-20 NUMBER OF SEQ ID NOS: 440
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
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CURRENT APPLICATION NUMBER: US/10/060,019
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TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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                                                                                                                   Application US/10060019 vo. US20030003564A1
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Milne, Todd
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Pred. No.
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APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7034
LENGTH: 387
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Best Local Similarity
Marches 12; Conserva
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; Sequence 1074, Application US/09925300
; Patent No. US20020151681A1
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                                                                                                                                                                                                                                                                             RESULT 32
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1074
                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
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SEQ ID NO 31
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PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR FILING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: US/09/177,165
PRIOR FILING DATE: 1998-10-22
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13; Conserv
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Pred. No.
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US-09-849-602-20
Sequence 20, Application US/09849602
Publication No. US20030165834A1
GENERAL INFORMATION:
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US-10-032-585-7788
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                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 7788
LENGTH: 511
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Matches
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                                           APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.
APPLICANT: Stockert, Elisabet
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000-
SOPTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
APPLICANT: Stockert, Elisabeth
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105(JRV)
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                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Candida albicans
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OTHER INFORMATION:
NAME/KEY: SITE
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NAME/KEY: SITE
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ORGANISM: Homo sapiens
FEATURE:
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Similarity 100.0%;
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Charles, Boone
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US-09-924-154-17, Application US/09924154; Sequence 17, Application US/09924154
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US-10-106-698-4938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Mammalian US-09-924-154-17
                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-01-03
NUMBER OF SEQ ID NOS: 8564
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LENGTH: 1501
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LENGTH: 725
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                                                                         SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4938
LENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4938, Application US/10106698 Publication No. US20030109690A1
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/924,154
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
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CURRENT FILING DATE: 2001-05-04
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SOFTWARE: PatentIn version 3.1
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APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
FILE REFERENCE: 05213-0465 43170-262105
FEATURE: MISC_FEATURE
                                       ORGANISM: Homo sapiens
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les 12; Conserv
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Pred. No. 0.052;
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                                                                                                                                                                                                              Sequence 36, Application US/10286264 Publication No. US20030093837A1 GENERAL INFORMATION:
                                                                             APPLICANT:
                                                                                                                   APPLICANT:
                                                                                                                                                      APPLICANT: Keddie, James
APPLICANT: Riechmann, Ju
APPLICANT: Ratcliffe, O
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Pineda, Omaira Heard, Jacqueline

Jiang Zhang, James

Cai-Zhong

Broun, Pierre Adam, Luc Yu, Guo-Liang Riechmann, Jose-Luis Ratcliffe, Oliver

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PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 462
LENGTH: 250
TYPE: PRT
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US-09-934-455-462
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                                                                                                                                   ; ORGANISM: Arabidopsis thaliana US-09-934-455-462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 462,
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Best Local
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CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
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APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
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                       502 NNNNNNNNNNN 512
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                                                              ch 0.9%; Score 11; 1 Similarity 100.0%; Pred. No. 11; Conservative 0; Mismatcl
4 NNNNNNNNNN 14
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Jiang, Cai-Zhong
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Riechmann, Jose Luis
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Ratcliffe, Oliver
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o. US20030121070A1
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/278,536
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 188
LENGTH: 298
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
FEATURE:
                              RESULT 40
US-09-991-496-134
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US-10-286-264-36
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Best Local Similarity 100.0%;
Matches 11; Conservative
Sequence 134, Application US/09991496 Patent No. US20020169285A1
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LENGTH: 298
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Best Local Similarity
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CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 165
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Broun, Pierre
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-011
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APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
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ORGANISM: Arabidopsis thaliana
FEATURE:
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TILE OF INVENTION: POLYNUCLEOTIDES FOR SEED TRAIT ALTERATION
                                                                                                   204 NNNNNNNNNS 214
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Ratcliffe, Oliver
Pilgrim, Marsha
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Reuber, Lynne
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Yu, Guo-Liang
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Search completed: October Job time : 102 secs
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CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 137
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 134
LENGTH: 309
TYPE: PRT
ORGANISM: Leishmania major and chagasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Gampos-Neto, Antonio
                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Shatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Branch, Mark
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C9
                                                                   256 FAYGQTGSGKT 266
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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[2]
REVISION TO 516.
TISSUE=Ovary;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REGULATES MICROTUBULE DYNAMICS DURING MITOTIC SPINDLE
-!- SUBCULIED FOR BOTH ESTABLISHMENT AND MAINTENANCE OF
MITOTIC SPINDLES. MAY ACT DIRECTLY ON MICROTUBULES, CAUSING A
DESTABILIZATION AND EVENTUAL DEPOLYMERIZATION OF THE MICROTUBULE.
-!- SUBCULIT BENEALING (POTENTIAL)

SUBCELLULAR LOCATION: Nuclear and cytoplasmic. SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2 SUBFAMILY.

mus musculu

PRINTS; PRO0386; KINESINHEAVY.

SMART; SM00129; KISc; 1.

PROSITE; PS00411; KINESIN\_MOTOR\_DOMAIN1; 1.

PROSITE; PS0041; KINESIN\_MOTOR\_DOMAIN2; 1.

PROSITE; PS0041; KINESIN\_MOTOR\_DOMAIN2; 1.

PROSITE; PS0041; KINESIN\_MOTOR\_DOMAIN2; 1.

PROSITE; PS0041; KINESIN\_MOTOR\_DOMAIN2; 1.

PROMAIN 1.

256 GLOBULAR (POTENTIAL).

DOMAIN 257 598 KINESIN-MOTOR (BY SIMILARITY).

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EMBL; U36485; AAC59743.2; -.
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Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISG; 1.

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A.; rotein that embly.";	KCMI. Xenopus laevis (African clawed frog). Xenopus laevis (African clawed frog). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus. NCBI_TaxID=8355; [1]	Created) Last sequence update) Last annotation update) 1 (XKCM1)	ALIGNMENTS PRT; 730 AA.	ALIGNMENTS	PTP3_DICDI RPB1_PLAFD KI21_STRPU	KF4A_MOUSE FL10_CHLRE	EG52_XENLA KF5C_HUMAN KINH_DROME	KF3A_MOUSE KF5C_MOUSE KF4A_XENLA	KF14_HUMAN
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Matches 175
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ISSUE=Kidney, and Uterus;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Shat N.K.,

Nleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Nleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Nleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Nleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Nleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Nleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Biochim.
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SEQUENCE
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(99661; Q96C18; Q96HB8; Q95HW8;

16-OCT-2001 (Rel. 40, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Kinesin-like protein KIF2C (Mitotic centromere-associated (MCAK) (Kinesin-like protein 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=T-cell;
MEDLINE=98094213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                Cheng L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim I.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Y., Sohn U., Kim Y.H.;
ression of human mitotic centromere-associated
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bukesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

C. centromeres at early prophase, and remains associated with the
cell cytler and prophase and remains associated with the
cell cytler and prophase and remains associated with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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IsoId=Q99661-2; Sequence=VSP 002866;
TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THYMUS AND TESTIS, AT LOW LEVELS IN SMALL INTESTINE, THE MUCOSAL LINING OF COLON, AND PLACENTA, AND AT VERY LOW LEVELS IN SPLEEN AND OVARY; EXPRESSION IS NOT DETECTED IN PROSTATE, PERIHERAL BLOOD LEUKOCYTES, HEART, BRAIN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, OR PAMCREAS.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic and nuclear ALTERNATIVE PRODUCTS:
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CONFLICT CONFLICT SEQUENCE NP\_BIND DOMAIN VARSPLIC Nuclear DOMAIN PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISC; 1. 88888 MIM; EMBL; U63743; AAC27660.1; -. EMBL; AY026505; AAK20168.1; EMBL; BC014924; AAH14924.1; EMBL; BC008764; AAH08764.1; PROSITE; PS00411; KINESIN\_MOTOR\_DOMAIN1; PROSITE; PS50067; KINESIN\_MOTOR\_DOMAIN2; Pfam; PF00225; kinesin; HSSP; P17119; 30; GO:000377; F:microtubule motor ac 30; GO:0003777; F:microtubule motor ac 30; GO:0008283; P:cell proliferation; 30; GO:007002; P:centromere binding; 30; GO:007067; P:mitosis; TAS. 11terPro; IPRO1752; Kinesin\_motor. DOMAIN MAIN 604538; protein; Microtubules; HGNC: 6393; protein; 449 698 255 618 348 415 A, Alternative KIF2C. 518 518 355 418 81312 ₹, complex; TAS s; ATP-binding; Coiled coil;
sy aTP-binding; Coiled coil;
ve splicing.
GLOBULAR (POTENTIAL).
KINESIN-MOTOR (BY SIMILARITY).
COILED COIL (POTENTIAL).
ATP (POTENTIAL). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MAMDSSLQARLFPGLAIKIQRSNGLIHSANVRTVNLEKSCV
SVEMARGGATKGKE -> M (in isoform 2).
/FTId=VSP 002866.
I -> L (IN REF. 1 AND 2).
R -> P (IN REF. 3; AAH08764).
55DECC133AB4B555C CRC64; motor activity; TAS ب ب

Query Match Best Local

Similarity

Length

725;

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RESULT 3
KF2C_MACFA
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28-FEB-2003
                                                                                                                                                                                                                                                                    TISSUE=Testis;
Hashimoto K., Osada
Terao K., Sugano S.,
                         use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                              libraries.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kinesin-like
                                                                                                                                                                                                                                                         'Isolation of novel full-length cDNA clones
                                                                                                                                                       centromeres at early prophase, and remains associated wi
centromere until after telophase (By similarity).
SUBCELLULAR LOCATION: CYtoplasmic and nuclear (By simila
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                             SUBFAMILY.
                                                                                                                                                                                                                  FUNCTION: Present
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(Rel. 41, Last annotation update)
protein KIF2C (Mitotic centromere-associated)
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BAB69716.1;
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42.1%;
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rly prophase, and remains associated with
                                                                                                                                                                                                                                                                                    Hida M.,
                                                                                                                                                                                                                                                                                                                                                                          eating macaque) (Cynomolgus monkey).
ata; Craniata; Vertebrata; Euteleostomi;
tes; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 752.5; DB 1;
Pred. No. 3.1e-26;
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                                       http://www.isb-sib
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RESULT 4
KIF2_HUMAN
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Best Local S
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                                                                                             SEQUENCE FROM N.A.
MEDLINE=97321046; PubMed=9177777;
Thermardi S., Fontanella E., de
                                                                                                                                                                                                                                15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                      KIF2_HUMAN
000139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
NP_BINI
                                                          cDNA differential display technique. Genomics 42:67-73(1997).
                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1. PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1. Motor protein; Microtubules; ATP-binding; C
                                                                                                                                                                                                         KIF2 OR KNS2.
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                                                                                                                                                        NCBI_TaxID=9606;
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Pfam; PF00225; kinesin; 1.
                                                                                  "Identification of a novel human kinesin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIND
          FUNCTION: THE KINESIN FAMILY MAY RECOGNIZE, TRANSPORTHEIR SPECIFIC CARGOES IN A SINGLE TYPE OF NEURONAL SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMISUBPAMILY.
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                                                                                                                                                                                                                   (Rel. 36, Created)
(Rel. 36, Last sequence up
(Rel. 36, Last annotation
protein KIF2 (Kinesin-2)
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464 K
604 C
301 A
75639 MW;
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Primates;
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KINESIN-MOTOR.
COILED COIL (POTENTIAL)
ATP (POTENTIAL).
                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                           Gregorio
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(1)
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No. 4.7e-26;
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a collaboration -

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KF2C CF
AC P70096
DT 01-NOV
DT 30-NAY
DT 30-NAY
DT 48-PEB
DE Kinesi
DE (MCAK)
GN KIF2C
OS Cricet
OC Eukary
OC Mammal
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the Euro
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DOMAIN
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SEQUENCE
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50067; KINESIN MOTOR Coiled coil; Neurone.

PROSITE; PS50067; KINESIN MOTOR (BY SIMILARITY).

DOMAIN 191 525 679 COILED COIL (POTENTIAL).

COLLED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
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HSSP; P17119; 3KAR.
                                     01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kinesin-like protein KIF2C (Mitotic centromere-
(MCAK) (Kinesin-like protein 6).
KIF2C OR KNSL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:6318; KIF2.
             Cricetulus griseus
Eukaryota; Metazoa;
                                                                                                           P70096;
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                                                                                                                                                                                 DLETQ
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(Chinese hamster).
; Chordata; Craniata; Vertebrata; Euteleostomi;
; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Pred. No. 1.6e
52; Mismatches
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   LRDIFVGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERIS
                                                    VVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGK
                                                                                                                                    ASRDVFLLKSOPRYRNLNL--
                                                                                                                                                           AAGDIFTF----
                                                                                                                                                                                TASNEVVÝRFTARPLVOTIFEGG-KATCFÁÝGÓTGSGKTHTMGGDLSGKSÓNTSKGÍYAM
                                         FSLVDLAGNERGADTSSADRQTRMEGAEINKSLLALKECIRALGQNKAHTPFRESKLTQV
                                                                                      QVVGLQEYLVNCADDVIKMLNMGSACKTSGQTFANSNSSRSHACFQILLR--AKGRLHGK
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LNIYDKDNTKGIFISFYEJYCGKLYDLLQKRKMVAALENGKKEV

----EVYVTFFEIYNGKVFDLLNKKAKLRVLEDSKQQV

294 481 234 423 174 370 122 311

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SEQUENCE FROM N.A.

MEDLINE=95122643; PubMed=7822426;

Wordeman L., Mitchison T.J.;

"Identification and partial characterization of mitotic associated kinesin, a kinesin-related protein that associent coentromeres during mitosis.";

J. Cell Biol. 128:95-105(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit.
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[1]
                                                                                                                                                                                                                                                                                                        PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U11790; AAB17358.2;
HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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centromere until after telophase.
SUBCELIULAR LOCATION: Cytoplasmic and nuclear.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Present
                                                                                                                                                                                                                                                                                                                                               ; PR00380; KINE; SM00129; KISC;
                                                              Similarity
                                                                                                                                                                                                                                                                  protein
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KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAR-1999)
                                             Conservative
                                                                                                                             Ŗ,
                                                                                                                                                                                                                                                                                       Microtubules;
                                                                                                                                                                                                                                                                                                                                                                    KINESINHEAVY.
                                                                                                                                                  248
512
651
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349
412
                                                                                                                             80918
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throughout the cell cycle, associated
rly prophase, and remains associated
                                                                                                                               ¥
                                             75;
                                           Score 735; DB 1;
Pred. No. 1.8e-25
5; Mismatches 13
                                                                                                                           ATP (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL
16ABD8BC66AD11B2 CRC64;
                                                                                                                                                                                   GLOBULAR (POTENTIAL).

KINESIN-MOTOR.

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                     ATP-binding;
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                                                                                                                                                                                                                                                                                       Coiled
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                                               136;
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RESULT
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RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Botherth A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-1693 (2002).

C. -I. SURCELLIAR IOCATION. Cytoplasmic and remains associated with the
centromere until after telophase (By similarity).
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as long as its commodified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or.send.an.email to license@isb-sib.ch).
             PROSITE; PS00411; KINESIN MOTOR DOWAIN1; 1
PROSITE; PS50067; KINESIN MOTOR DOWAIN2; 1
Motor protein; Microtubules; ATF-binding;
                                                                                                                        MGD; MGI:1921054; Kif2c.
InterPro; IPR001752; kinesin_motor.
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Mammalia; Eutheria;
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28-FEB-2003
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15-SEP-2003
Nuclear
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SIMILARITY: BELONGS TO
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                                                                                                              PF00225; kinesin;
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                                                                         SM00129; KISC;
                                                                                        PR00380; KINESINHEAVY
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
protein KIF2C (Mitotic centrome
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Feingold E.A., Grouse L.H.,
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic and nuclear
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(Mitotic centromere-associated
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Mullahy S.J.,
naratne P.H.,
J., Hulyk S.W.,
                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scheetz T.E.,
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DOMAIN
NP_BIND
                                                                                                                                                                                         "Kinesin family in murine central nervous system.";

J. Cell Biol. 119:1287-1296(1992).

I. FUNCTION: THE KINESIN FAMILY WAY RECOGNIZE, TRANSPORT AND POSITIO

I. FUNCTION: THE KINESIN FAMILY WAY RECOGNIZE, TRANSPORT AND POSITIO

THEIR SPECIFIC CARGOES IN A SINGLE TYPE OF NEURONAL CELL.

ITS EXPECIFICITY: EXPRESSED AMONG VARIOUS TISSUES UBIQUITOUSLY;

ITS EXPRESSION LEVEL IN BRAIN DECREASES WITH DEVELOPMENT.

ITS EMPLIARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
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15-SEP-2003
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                                                                                                                       This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                   Hirokawa N
                                                                                                                                                                                                                                                                                                                                                                                          Aizawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93077686;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIF2 OR KIF2A OR KNS2.
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(Rel. 24, Last sequence update)
(Rel. 42, Last annotation update)
protein KIF2.
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Y., Takemura R.,
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Pred. No. 2.
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KINESIN-MOTOR (BY SIMILA
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
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01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Kinesin-like protein KIF2C (Mitotic centromere-associated
                                              Sperry A.O., Zhao L.-r.,
Sperry A.O., Zhao L.-r.,
Whinesin-related proteins in the
"Kinesin-related proteins in the
for meiosis and morphogenesis.",
Mol. Biol. Cell 7:289-305(1996).
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SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Tes
MEDLINE-96228687; PubMed-8688559;
Sperry A.O., Zhao L.-P.;
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PIR; A
HSSP;
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

Motor protein; Microtubules; ATP-binding; Coiled coil; Neur
MOTOR PROTEIN; MICROTUBULER; ATP-BINGER (POTENTIAL).

DOMAIN 1 189 GLOBULAR (POTENTIAL).

DOMAIN 190 539 KINESIN-MOTOR (BY SIMILARITY).
    Sperry A.O.;
                                                                                                                                                                                                                               NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                             REVISIONS
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SM00129; KISC; 1.
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Rodentia;
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ATP (BY SIMILARITY).
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Sciurognathi; Muridae;
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PIR; T10755; T10755.
HSSP; P17119; 3KAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00411; KINESIN MOTOR DOMAIN1; PROSITE; PS50067; KINESIN MOTOR DOMAIN2; MOTOR protein; Microtubules; ATP-binding;
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Pfam; PF00225; kinesin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Present throughout the cell cycle, associates with centromeres at early prophase, and remains associated with the centromere until after telophase (By similarity). Active in
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  TEEMDASS
                                              GSEMNASSIENVVIKSNHLLSNNNNNKIN--RGKINDKIERNNILKNKSFDKPRE
                                                                                                                        VGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSK
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78; Mismatches
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Coiled Motor protein; Microtubules; ATP-binding; Coiled DOMAIN 1 192 GLOBULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96140638; PubMed=8548824; Walczak C.E., Mitchison T.J., Desai A.; Walczak C.S., Mitchison T.J., Desai A.; "XKMMI: a Xenopus kinesin-related protein that dynamics during mitotic spindle assembly.";
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                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00225; kines
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HSSP; P17119; 3KAR.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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431
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                                                               LKILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAF
                                                                                                                                                     TAPNETVYRFTARPLVETIFERG-MATCFAYGQTGSGKTHTMGGDFSGKNQDCSKGIYAL
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                       IDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRD
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IDLAGNERGADTSSADRQTRLEGAEINKSLLALKECIRALGRNKPHTPFRASKLTQVLRD
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682 AA;
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KIF2 (Kinesin-related pr
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Asparagine-rich protein (AG319) (ARP)
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Brown G.V., Anders R.F., Kemp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96222363; PubMed=8636234; Wein H., Foss M., Brady B., Cande W.Z.; "DSKI, a novel kinesin-related protein from the diator fusiformis that is involved in anaphase spindle elongy J. Cell Biol. 133:595-604(1996).

-:- FUNCTION: INVOLVED IN ANAPHASE SPINDLE ELONGATION
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01-NOV-1997 (Rel. 35, I
01-NOV-1997 (Rel. 35, I
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Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Bacillariales; Bacillariaceae; Cylindrotheca.
NCBI_TaxID=2853;
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HSSP; P17119;
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                                                                                                                                                                                                                                    PF00225; kinesin;
   Similarity
                                                                     PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Octein; Microtubules; ATP-binding; Coiled coil.
1 85 GLOBULAR (POTENTIAL).
1 86 425 KINESIN-MOTOR (BY SIMILARITY).
426 624 COILED COIL (POTENTIAL).
186 193 ATP (POTENTIAL).
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IPR001752; kinesin_motor.
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576; DB 1;
No. 1.3e-18;
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RESULT 12
KIP1_YEAST
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SEQUENCE FROM
STRAIN=S288c;
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"Kinesin-related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharo
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15-JUL-1998
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01-DEC-1992
                                                                                                mitotic spindle."
                                                                                                                 Saunders W.S., Hoyt M.A.;
"Kinesin-related proteins
                                                                                                                                                     STRAIN=S288c;
MEDLINE=92354062;
                                                                                                                                                                                                                                                                                                  Scherens
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                                                                                                                                                                                                                                                                                                                                                                                                     spindle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinesin-like
                                                                                                                                                                                        CHARACTERIZATION
                                                                                                                                                                                                                      MEDLINE=94205266; PubMed=8154187;
Scherens B., el Bakkoury M., Vierendeels F., Dubois E.,
"Sequencing and functional analysis of a 32,560 bp segme
left arm of yeast chromosome II. Identification of 26 op
frames, including the KIP1 and SEC17 genes.";
"Yeast 9:1355-1371(1993).
     otic spindle.";
170:451-458 (1992).
170:451-458 (1992).
FUNCTION: REQUIRED FOR ASSEMBLY OF THE MITOTIC SPINDLE. INTERACT FUNCTION: REQUIRED FOR ASSEMBLY OF THE MITOTIC SPINDLE ASSEMBLY, CINE AND WITH SPINDLE MICROTUBULES TO PRODUCE AN OUTWARDLY DIRECTED AND WITH SPINDLE ASSEMBLY, CINE AND TOTAL TRANS SEPARATED POLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sin-like protein KIP1.
OR CIN9 OR YBL063W OR YBL0504 OR
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EMBL; Z32661; CAA80785.1; -.
EMBL; Z35624; CAA84883.1; -.
PIR; A42640; A42640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
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SGD; S0000159; KIP1.
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94 MW; 212F8279766137FC CRC64;
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Pred. No. 1e-17;
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RESULT 13

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PT 01-AUG-1992 (Rel. 2:

DT 01-BUG-1992 (Rel. 2:

DT 15-BEC-1998 (Rel. 3:

DNA-directed RNA po

CE Lukaryota; Alveelat.

OX NCBI_TAXID=5833;

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RT Plasmodium falcipar

MO1. Biochem. Paras

CC -1- FUNCTION: DNA-D

CC OF DNA INTO RNA

CC -1- CATALYTIC ACTIV

CC -1- SUBUNIT: RNA PO
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                                                                          Plasmodium falciparum RNA polymerase III.";
Mol. Biochem. Parasitol. 46:229-240(1991).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92018020; PubMed=1656254;
Li W.B., Bzik D.J., Tanaka M., Gu H., F
"Characterization of the gene encoding"
                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase III largest subun
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemospori
      SUBSTRATES.
- CATALYTIC ACTIVITY: N
{RNA}(N).
- SUBUNIT: RNA POLYMER!
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Best Local Similarity
Matches 356; Conserv
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InterPro; IPR007080; RNA pol Rpbl 1.

InterPro; IPR007066; RNA pol Rpbl 3.

InterPro; IPR007066; RNA pol Rpbl 4.

InterPro; IPR007083; RNA pol Rpbl 5.

InterPro; IPR007081; RNA pol Rpbl 1.

InterPro; IPR006592; RNA pol Rpbl 1; 1.

Pfam; PF04997; RNA pol Rpbl 2; 1.

Pfam; PF04983; RNA pol Rpbl 3; 1.

Pfam; PF05000; RNA pol Rpbl 3; 1.

Pfam; PF05000; RNA pol Rpbl 3; 1.

Pfam; PF04998; RNA pol Rpbl 3; 1.

SMART; SM00663; RNA pol Rpbl 5; 1.

SMART; SM00663; RNA pol Rpbl 5; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger; Nuclear protein.
ZN_FING 88 101
SEQUENCE 2339 AA; 272829 M
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MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR SS AND TRNA GENES.

SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF
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FDKPREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLY-NDNTINKKHNNNNNNNNNNNDN | :: | :: | | | | | | :: | | :: | | :: |
                                                                                                                          ----SCDKQIVQFI-YGDDALNPSYIDNNNTYLDQFDKVFDHIVSISSSHLLLSYKNK
                                                                                                                                                          NISPTISCCEQTLNTLRYSSRVKN---FKNKSTCINEEDDTNTERISILDS-----
                                                                                                                                                                                             VQNSFYTGLSPTEFFFHTMSGREGLVDTAVKTAETGYMQRRLMKALEDLSIHYDYSVR--
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                                                                                   KGSEMNASSIENVVIKSNHLLSNNNNNKINRGKI-NDKIERNNILKNKS
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Pred. No. 2.5e
234; Mismatches
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                                                    --IYNN--MNNINNNDSNRSIIYNNDSNMNNINNNDS
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Pfam; PF00122; E1-E2_ATPase; 1.
TIGRRAMs; TIGR01494; ATPase_P-type; 7.
PROSITE; PS00154; ATPASE_E1_E2; 1.
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J. Cell Biol. 120:385-398(1993).
J. Cell Biol. 120:385-398(1993).
J. Cell Biol. 120:385-398(1993).
J. CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
J. SUBCELLULAR LOCATION: Integral membrane protein.
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STRAIN=T9/96;
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Eukaryota; Alveolata;
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39, Last sequence update)
42, Last annotation update)
ransporting ATPase 1 (EC 3.6.3.-).
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CYTOPLASMIC (BOTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

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    --NKNTSNIQNINTNK---
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Pred. No. 1.2e-16;
2; Mismatches 412;
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W; AE708AAE99009335 CRC64;
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MEDLINE=21848401; PubMed=11859360;
MODDINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
James K., Jones C., Jones M., Leather S., McDonald S., McLean J.,
James K., Jones G., Mindall K., Murphy L., Niblett D., Odell C.,
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P24339;
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01-0CT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Kinesin-like protein cut7.
CUT7 OR SPAC25G10.07C.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
As Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
As Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithead S.,
As Weltjers I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
As Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
As Horzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
As Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
As Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
As Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
As Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
As Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
As Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
As Daga R.R., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G.,
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As Cernutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: COULD BE A SPINDLE POLE BODY MOTOR. ON TRANSITION FROM G2 TO M PHASE OF THE CELL CYCLE, THE SPINDLE POLE BODY DUPLICATES; THE DAUGHTER POLE BODIES SEED MICROTUBLIES WHICH INTERDIGITATE TO FORM A SHORT SPINDLE THAT ELONGATES TOSPAN THE NUCLEUS AT METAPHASE. MUTATIONS AT CUT7 BLOCK SPINDLE FORMATION. SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
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밁 Ś В Ś Query Match Best Local S Matches 235 EMBL; X57513; CAA40738.1; -.
EMBL; Z70691; CAA94636.1; -.
PIL; T38378; T38378.
HSSP; P17119; 3KAR.
GeneDB SPombe; SPAC25G10.07c; InterPro; IPR001752; kinesin\_mo
Pfam; PF00225; kinesin; 1. CONFLICT DOMAIN
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REPEAT DOMAIN DOMAIN PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
Motor protein; Cell division; Microtubules; ATP-binding; PRINTS; PR00380; KINE SMART; SM00129; KISC; SEQUENCE MOD\_RES 121 56 71 w Similarity AFDKVFGPEADQLMLFENSVAPMLEQVL-NGYNCTIFAYGQTGTGKTYTMSGD----LSD IVDKVFDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGOTGSGKTYTMLGSQPYGQSD SKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYID-----5801 70 436 715 715 897 159 987 999 Conservative 34 cycle; AA, KINESINHEAVY 435 604 740 955 1010 61 20.7%; 122133 Phosphorylation; 7.9%; 223; Æ; \_motor Pred. PHOSPHORYLATION (BY CDC2) (B: SIMILARITY). SASNPRKRREPPTIDTGYPDRSDTNSPT LRAILGNDVSLLLLTL (IN REF. 1) COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (BY SIMILARITY). Score 538.5; KINESIN-MOTOR (BY SIMILARITY) Mismatches 5669277875559D58 No. VRDNSSLAVSTSGAMGAELAI QSDPSSMLVTKTY Repeat 1e-16 DB 1; 410; Indels Length CRC64; -EPRYKVDMTKYIERHEF Coiled coil; 265; Gaps

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                                                                                                                                                                                SKRELPATPSWTRDSSLIKETTNLN--LDSDKKFVRETYTSSNQTNEPDVYDK
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SEQUENCE
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MEDLINE-2003487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V. Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: RESPONSIBLE FOR MICROTUBULE TRANSLOCATI IMPORTANT FOR THE ORGANIZATION OF PHRAGMOPLAST-SP MICROTUBULES (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED (BY -!- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED (BY -!- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED (BY -!- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED (BY -!- SUBCELLULARITY: BELONGS TO THE KINESIN-LIKE PROTEIN F
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Probable 1.25 kDa kinesin-related protein.
AT2G36200 OR F2H17.19
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                               SAQQKDLYDQAVVPIVNEVLE-GFNCTIFAYGQTGTGKTYTMEGECRRSKSAPCGGLPAE
PLMEDGKGGVLVRGLEEEIVTSANEIFTLLERGSSKRRTAETFLNKQSSRSHSLFSITI-
                                                                                                                                                                                                                                                                                                   TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                            IKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMT-KYIERHEFIVDKVFDD
                                                                                                                  AGVIPRÁVKQÍFDTĹE--GQQAEYSVKVTFLELÝNEEITDĹĹAPEDLSRVAAEEKQKKPL
                                                                                                                                                                           PGIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLL-----
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COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
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E., Feldblyum T.V.
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023826;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
125 kDa kinesin-related protein.
    Nicotiana tabacum (Common Eukaryota; Viridiplantae;
                                                                                        TKRP125.
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CHARACTERIZATION.

STRAIN=cv. Bright Yellow 2;

STRAIN=ev. Bright Yellow 2;

MEDLINE=97196959; PubMed=99044048;

MEDLINE=97196959; PibMed=9044048;

MEDLINE=97196959; PibMed=97196959;

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[1]
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STRAIN=cv.
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J. Cell Sci. 107:2249-2257(1994)
-i- FUNCTION: RESPONSIBLE FOR MICROTUBULE TRANSLOCATION. MAY BE IMPORTANT FOR THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPRETANT FOR THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OF PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OR PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OR PHRAGMOPLAST-SPECIFIC ARRITMOPLES OF THE ORGANIZATION OR PHRAGMOPLAST OR THE ORGANIZATION OR PHRAGMOPLAST OR THE ORGANIZATION OR PHRAGMOPLAST OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE OREAL ORGANIZATION OR THE ORGANIZATION OR THE ORGANIZATION OR THE O
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Coiled DOMAIN 1 359 KINESIN-MOTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Asada T., Shibaoka H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Motor protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001752; kinesin_motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
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BEVELOPMENTAL STAGE: EXPRESSED DURING S PHASE. EXPRESSION

DEVELOPMENTAL STAGE: EXPRESSED DURING S PHASE.

INCREASES AS CELL MOVES FROM S PHASE TO M PHASE AND THEN DECH

RAPIDLY AS CELL ENTERS THE G1 PHASE. EXPRESSION INCREASES AGA

DURING THE G2 PHASE.

SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
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ATP (BY SIMILARITY).
T -> Q (IN REF. 1; AA SEQUENCE)
E -> P (IN REF. 1; AA SEQUENCE)
D -> Q (IN REF. 1; AA SEQUENCE)
MW; 890C0E0F3504AA7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 513; DB 1;
Pred. No. 1.2e-15;
9; Mismatches 379
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01-MAY-1991
01-MAY-1991
01-NOV-1995
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microrubules; ATP-binding; Coiled DOMAIN
1 385 KINESIN-MOTOR (BY S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=90153980; PubMed=2137456;

Kosik K.S., Orecchio L.D., Schnapp B., Inouye H.,

"The primary structure and analysis of the squid )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loligo pealeii (Longfin squid).
Bukaryota; Metazoa; Mollusca; Cephalopoda;
Decapodiformes; Loliginidae; Loligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J05258; AAA29990.1; PIR; A35075; A35075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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Pfam; PF00225; kinesin; 1.
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FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN THAT MAY PLAY A ROLE IN ORGANIELLE TRANSPORT.
SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
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217; Conservative
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                                                                  RIVQDIFNYIYGMDENLEFHIKISYYEIYLDKIRDLLDVTKTNLAVHEDKNRVPFVKGAT
                                                                                                        YAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKI
                                                                                                                                                                           VDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQFYGQSDTP---
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(Rel. 32,
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, Last seq
, Last ann
-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTS---LGKIAF
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Pred. No. 4e-19
89; Mismatches
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MICROTUBULE-BINDING.
ATP (BY SIMILARITY).
WW; CC40353FA3F33E35 C
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(See http://www.isb-sib.ch/announce/
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SIMILARITY).
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KINESIN CHAINS)

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RN SEQUEN
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01-AUG-1990
01-AUG-1990
01-NOV-1997
SEQUENCE FROM N.A.
MEDLINE=90199865; PubMed=2138511;
Enos A.P., Morris N.R.;
"Mutation of a gene that encodes
                                                                                              Emericella nidulans (Aspergillus nidulans)
Eukaryota; Fungi; Ascomycota; Pezizomycoti
Eurotiales; Trichocomaceae; Emericella.
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15, Last sequence update)
35, Last annotation updat
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                                                                                                                Pezizomycotina;
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    kinesin-like protein
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Matches 253
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nuclear division in A. nidulans.";
Cell 60:1019-1027(1990).
Cell FORCTION: IMPORTANT ROLE IN MITOTIC DIVIDING
MOTOR REQUIRED FOR SPINDLE BODY SEPARATION.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1. PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1. Motor protein; Cell division; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00380; KINE:
SMART; SM00129; KISC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
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Pfam; PF00225; kinesin; 1:
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      VLONTRAQLEEEEMLRCAHEETEHQLQDVGKGLISTLGQTVEDINSLQSK--
                                       IKKNKK---
                                                                    RRIISEEQRAKIESMESSLRHKVQELLTLTSK-FNDLKKDNDDTLAALCSTNDVLQQTDI
                                                                                               NHLLSNNNNNKIN--RGKINDKIERNNILKNKSFDKPREGFTSTFGKYSSLNDI----
                                                                                                                                AKNIRNKPQ-INSTMPKMTLLREFTAEIEKLKAELIATRHRNGVYMSVESYEEMKMENES
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MW; CEA015E
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Pred. No. 5.3e-15;
4; Mismatches 415
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COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
ATP (BY SIMILARITY).
PHOSPHORYLATION (BY CDC2) (BY
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                                     KGLIN-YKSTLYNDNTINKKHNNNNNNNND
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01-JUL-1993
30-MAY-2000
                                                                                               Nature
[2]
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                        MEDLINE=93024922; PubMed=1406971;
Yen T.J., Li G., Schaar B.T., Szilak
"CENP-E is a putative kinetochore mot
                     microtubule motor
                        Thrower D.A., Jordan M.A., (
"Mitotic HeLa cells contain microtubule motor.":
                                                                                                                              mitosis
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  Centromeric
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                                                                             CHARACTERIZATION.
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    14:918-926(1995)
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(Rel. 26, Last sequence update)
(Rel. 39, Last annotation update)
protein E (CENP-E protein).
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                             PubMed=7889940;
dan M.A., Schaar B.T., Yen T.J.
ls contain a CENP-E-associated
                                                                                                                                                                                                                                     Chordata;
Primates;
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CHARACTERIZATION.
MEDLING=98437347; PubMed=9763420;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;
Characterization of the kinetochore binding domain interactions with the kinetochore proteins CENP-F ar J. Cell Biol. 143:49-63(1998).

J. Cell Biol. 143:49-63(1998).

J. Cell Biol. 143:49-63(1998).

J. Cell Biol. 143:49-63(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
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PIR; S28261; S28261.
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GO:0005634;
GO:0008350;
GO:0000067;
GO:0007079;
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SUBCUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE. SUBCULIAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION. SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
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C:nucleus; TAS.
F:kinetochore motor activity;
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Pred. No. 7.3e
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ATP (BY SIMILARITY).
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es 612;
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	RN [2]  RP SEQUENCE FROM N.A.  RC STRAIN=Berkeley;  RX MEDLINE=20196006; PubMed=10731132;  RAdams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,  RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  RA Brandon R.C., Rogers YH.C., Blazej R.G., Champe M., Pfeiffer B.D.,  RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  RA Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch C., Baldwin D.,  RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	SULT 21  FACASON STATE OF THE S	Qy 1113

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"The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0004381; Klp68D.
GO; GO:0003774; F:motor activity; IDA.
GO; GO:0008089; P:anterograde axon cargo
InterPro; IPR001752; kinesin motor.
Pfam; PF00225; kinesin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart R.J., Pessavento P.A., Woerpel D.N., Goldstein L.S.B.;
"Identification and partial characterization of six members of the
kinesin superfamily in Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).
-!- FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED F
ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES
FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OF
                                                                                                                                                                                                                                                                       PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules, ATP-binding; Coiled coil.
DOMAIN 16 275 KINESIN-MOTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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GSRAK -> VRGQV (IN REF. 3).
G -> A (IN REF. 2).
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Pred. No. 3.4e-14;
0; Mismatches 291
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large proteins in vitro.";
4:141-150(1997).
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KF3B_HUMAN
015066;
15-DEC-1998
Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. V. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.":
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                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                               MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                    TISSUE=Brain;
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Primates;
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annotation update)
(Microtubule plus
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L., RA Bailey J., Batrow K.F., Bates K.N., Beard L.M., Beare D.M., Balley J.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Carder C., Carter N.P., Clark S.Y., Clee C.M., RA Beasley O.P., Burler A.P., Carder C., Carter N.P., Clee C.M., RA Chegg S., Cobley V.E., Collier R.E., Connor R.B., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., RA Clegg S., Cobley V.E., Collier R.E., Connor R.B., Corby N.R., RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Huckle E., Hunt A.R., King A., Knights A., Laird G.K., Lawlor S., Laird G.K., Lawlor S., Laird G.K., Lawlor S., Lake M.J., Lovell J.D., Marsh V.L., Matrin S.L., McConnachie L.J., McLay K., McMurray A.A., RA Mille S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., RA RA R.C. C.M., ROSS M.T., Sooder J.M., Shownkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.M., Thorpe A., RA Millenad S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., RA Store C. W., Kray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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SEQUENCE FROM N
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J. Biol. Chem. 273:6591-6594 (1998).

-!- FUNCTION: Involved in tethering the chromosomes to the spindle pole and in chromosome movement. Microtubule-based anterograde translocator for membranous organelles. Plus end-directed microtubule sliding activity in vitro (By similarity).

-!- SUBUNIT: Heterodimer of KIF3A and KIF3B (By similarity). Interior of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                  88888
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EMME, AL121897; CAC16425.1; -.
HSSP; P17119; 3KAR.
Genew, HGNC:6320; KIF3B.
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                                                               Motor
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                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005873; C:plus-end kinesin complex; TAS.
GO:0005877; F:microtubule motor activity; TAS.
GO:0003777; F:plus-end-directed kinesin ATPase activity;
GO:0008574; F:plus-end-directed kinesin ATPase activity;
GO:0008089; P:anterograde axon cargo transport; TAS.
GO:0007368; P:determination of left/right asymmetry; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is pween the Swiss Institute of Bioinformat European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
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re 414:865-871(2001).
                                                                                                 protein;
                                                                                                                                                                                                                                         SM00129; KISc;
PS00411; KINESIN MOTOR_DOMAIN1; 1.
PS50067; KINESIN MOTOR_DOMAIN2; 1.
Cotein; Microtubules; ATF-binding; Coiled coil; Neurone.
1 345
KINESIN-MOTOR (BY SIMILARITY).
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COILED COIL (BY SIMILARITY).
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(See http://www.isb-sib.ch/announce/
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RESULT 23
KF3B_MOUSE
ID KF3B_MOU
AC Q61771;
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Mammalia; E
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                                                                          microtubule
transport.";
                                                                                  MEDLINE=96032268; PubMed=7559760;
Yamazaki H., Nakata T., Okada Y., Hirokawa N.;
"KIF3A/B: a heterodimeric kinesin superfamily
microtubule plus end-directed motor for membra
                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                     motor 3B).
                                                                                                                                                                                                                               Kinesin-like
                                                                                                                                                                                                                                                   15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                               STRAIN=ICR;
                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                          KIF3B
                                                                                                                                                                                                                                        15-SEP-2003
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         pole and in chromosome movement. Microtubu
translocator for membranous organelles. Pl
microtubule sliding activity in vitro (By
SUBUNIT: Interacts with the SMC3 subunit
                                                     FUNCTION: Involved
                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  282
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                                                               Biol.
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                                                                                                                               FROM N.A.
CR; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                        NHIPPRDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLDGENHIRVGKLNLVDLAGSERQAKTGAQGERLK-EATKINLSLSALGNVISALVDGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --DINKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAM-DSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGKKEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGQSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQK--RKWVAALE
                                                                                                                                                                                                                                                                                                                                         RRKRREKRREG
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                                                                                                                                                                         ; Metazoa;
Eutheria;
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(Rel.
(Rel.
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Rodentia;
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KIF3B
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                                                    tethering the chromosomes
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                                                                                                                                                                                                                                                    sequence update)
                                                                                                                                                                                                                             annotation update)
(Microtubule plus
  the SMC3 subunit of th . Heterodimer of KIF3A
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POLY-SER.
; 97FA4573AFA87023 CRC64;
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                                                                                                                                                                         Craniata; Vertebrata; l
Sciurognathi; Muridae;
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nelles. Plus end-directed
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                     similarity)
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; Murinae; Mus
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                                            anterograde
                                                      spindle
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recycling.

protein, Won

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Kin

H.B.;

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RESULT 24
KLP3 SCHPO STANDARD;
ID KLP3 SCHPO STANDARD;
AC Q9US60; Q9US61;
DT 16-OCT-2001 (Rel. 40, Created)
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOR_DOMAIN2; 1.
MOTOR_DOMAIN2; 1.
MOTOR_DOMAIN 1 345
KINESIN-MOTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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InterPro; IPR001752; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A57107; A57107.
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SM00129; KISC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 472.5; DB 1;
Pred. No. 5.1e-14;
4; Mismatches 148;
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         RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Kelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gorzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gorffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002).
CC MRNRANE REGYCLING.

CC MRNRANE REGYCLING.
                          EMBL; AF154055; AAF14525.1; --
EMBL; AF156966; AAF22609.1; --
EMBL; AF247188; AAF81205.1; --
EMBL; AL157734; CAB75775.1; --
PIR; T50118; T50118.
                                                                                                                                                            use by non-profit institutions as long as modified and this statement is not removed. I entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are in the European Bioinformatics Institute.
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"A fission yeast kinesi
Yeast 16:149-166(2000).
[2]
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Brazer S.-C.W., Williams H.P., Chappell T.G., Ca
"A fission yeast kinesin affects Golgi membrane
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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28-FBB-2003 (Rel. 41, Last annotation update
Kinesin-like protein 3 (Kinesin-related pro-
KLP3 OR KRP1 OR SPAC1834.07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M
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                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
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PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

ATP-binding; Coiled coil; Motor protein.

ATP-binding; 1 332

CTMTLARTY).
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pfam; pf00225; kinesin; 1.
prixTS; pr00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
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Pfam; PF00792; PI3K C2; 1.
Pfam; PF00794; PI3K Tbd; 1.
Pfam; PF00613; PI3Ka; 1.
Pfam; PF00613; PI3Ka; 1.
SMART; SM00142; PI3K Tbd; 1.
SMART; SM00144; PI3K Tbd; 1.
SMART; SM00146; PI3KC; 1.
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Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
"A phosphatidylinositol (PI) kinase gene family in Dictyostel discoideum: biological roles of putative mammalian p110 and y Vps34p PI 3-kinase homologs during growth and development.";
Mol. Cell. Biol. 15:5645-5656(195).
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 1-phosphatidyl-1D-myo-inositol 3-phosphatidyl-1D-myo-inositol SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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PIKC OR PIK3.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dic
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InterPro, IPR002420; PI3K_C2.
InterPro, IPR000341; PI3K_ras_bind.
InterPro, IPR001263; PI3Ka.
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PS00916; PI3_4_KINASE_2; 1.
PS50290; PI3_4_KINASE_3; 1.
ase; Kinase; Multigene family;
                      KSFDKPREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYNDNTINKKHNNNNNNND
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Dictyosteliida; Dictyostelium
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                                             Score 465.5;
Pred. No. 2.3e
)3; Mismatches
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les 212;
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01-AUG-1992
01-FEB-1995
15-SEP-2003
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01-FEB-1995 (Rel. 31, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Kinesin-like protein CIN8.
CIN8 OR KSL2 OR YEL061C.
                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycessaccharomycetales; Saccharomyces
                                                                         "Two Saccharomyces cerevisiae kinesin-related for mitotic spindle assembly.";
J. Cell Biol. 118:109-120(1992).
                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=S288C;
  STRAIN=S288c / AB972;
                           SEQUENCE
                                                                                                                                              MEDLINE=92317149; PubMed=1618897; Hoyt M.A., He L., Loo K.K., Saund
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PIR; S50528; B42641.
HSSP; P17119; 3KAR.
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Motor_protein; Cell division; Microtubules;
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GO; GO:0000092; P:mitotic anaphase
InterPro; IPR001752; kinesin_motor.
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ROUSSelet G., Simon M., Ripoche P., Buhler J.M.;
"A second nitrogen permease regulator in Saccharomyces FEBS Lett. 359:215-219(1995).
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SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
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                                 IYNNINDDDTFQNDYCHNDNTFTIRKKNNTNINSNIYQNDDIIYTINSLNDYMSNTLLHF
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Kinesin-like protein KIF3A (Microtubule plus
                                                                                                                                                                     InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                EMBL; AF041853; AAC72294.1; HSSP; P17119; 3KAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burnside B.;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      motor 3A).
                                                                                                                                                                                                                  GO; GO:0006996; P:organelle
                                                                                                                                                                                                                                       Genew; HGNC:6319;
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Whitehead J.L., Wang S.Y., Bost-Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Pred. No. 1.7e-13;
4; Mismatches 192
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MEDLINE=2196006; PubMed=10731132;

MEDLINE=2196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopteryota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                   STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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Nature 398:225-225(1996).
-!- FUNCTION: IMPORTANT ROLE IN MITOTIC DI
MOTOR REQUIRED FOR SPINDLE BODY SEPARAS.
MICROTUBULE MOTOR CAPABLE OF CROSS-LIN
ANTIPARALLEL MICROTUBULES, THEREBY PUS
SPINDLE POLES DURING SPINDLE ASSEMBLY
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Misra S., c.,
Hradecky P., J
Tmith C.D., 7
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                                                                                                                                                                                                                                                                                                                                STRAIN=DP CN BW;
MEDLINE=92020874; PubMed=1924306;
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MEDLINE=22426066; PubMed=12537569;
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                                                                                                                                                                                                                                                                             kinesin
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                  George R.A., Guarin H., Kronmiller B., Pac
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
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Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Annotation
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01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kinesin heavy chain (Ubiquitous kinesin heavy
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Kull F.J., Sablin
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Mammalia; Eutheria;
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J. Cell Biol. 117:1263-1275(1992).
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                                                                                  rity to myosin.";
380:550-555(1996)
                                                                                                          y6.195066; PubMed=8606779;
., Sablin E.P., Lau R., Fletterick R.J.,
structure of the kinesin motor domain re
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   PubMed=7514426;
F., Hom-Booher
                                                                                                                                                                                                                                                                                                               PubMed=1607388;
J., Hom-Booher
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Neuron 12:1059-1072(1994).

-i- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED PROTEIN THAT MAY PLAY A ROLE IN ORGANIELE TRAN -:- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS
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PROSITE; PSO0467; KINESIN MOTOR DOMAIN2; 1.

MOTOR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN; 1256

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GG; GO:0004002; F:adenosinetriphosphatase acti
GG; GO:0003777; F:microtubule motor activity;
GG; GO:0007018; P:microtubule-based movement;
InterPro; IPR001752; kinesin motor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND THE PROCESSES IN T
TISSUE SPECIFICITY: FO
KIDNEY, SPLEEN, HEART,
DOMAIN: COMPOSED OF TH
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PIR; S64238; S6422...
PIR; S64238; S6422...
HSSP, P17119; 3KAR.
SGD; S0003184; KIP3.
G0; G0:0005881; C:ccytoplasmic microtubule; IDA.
G0; G0:0005880; C:nuclear microtubule IDA.
G0; G0:0005881; P:microtubule depolymerization; IMP.
G0; G0:0005881; P:mitotic spindle assembly (sensu Sacchařomyces); IGI
G0; G0:000013; P:mitotic spindle orientation; IGI.
G0; G0:000013; P:mitotic spindle orientation; IGI.
G0; G0:000015; P:nuclear migration (sensu Saccharomyces); IMP.
T=P2F70; IPR001752; Kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ly96 (Rel. 34, La
Lu-FEB-2003 (Rel. 41, Lau
Kinesin-like protein KIP3
KIP3 OR YGL216W.
Saccharomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIP3_YEAST
P53086;
                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of 20 chromosome VII."; Yeast 13:1077-1090(1997)
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97435481; PubMed=9290212;
Rieger M., Brueckner M., Schaefer M., Mu
"Sequence analysis of 203 kilobases from
                                                                                                                                                                                                                               or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; /
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                            modified
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cetaceae; Saccharomyces.
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O14343;
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Motor protein; Microtubules; ATP-binding; Coiled coil.

DOMAIN 1 436

DOMAIN 449 481

COILED COIL (POTENTIAL)

NP BIND 192 199

ATP (POTENTIAL)

SEQUENCE 805 AA; 91000 MT
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Pred. No. 4.1e-13;
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HSVGSKLTMF

563 502 509 486 452 394 378 277 224

164 204 107 23

SNSIYK

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Holroyd S., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., Mollett D., Odell C.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Hushlett D., Odell C.,
RA Willer S., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Kelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Weltjend J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Meller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Charlet B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002)
                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                     EMBL; AB072924; BAB69885.1; EMBL; Z97211; CAB10160.1; -PIR; T40128; T40128.
                          GeneDB_SPombe; SPBC2F12.13; -.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Two kinesin-like Kin I family proteins in fission yeestablishment of metaphase and the onset of anaphase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Two kinesin-like Kin I far
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401;
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                                                                                                                          HSSP; P17119; 3KAR
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28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 during kinetochore capturing.
SUBUNIT: Heterodimer with klp6.
SUBCELLULAR LOCATION: Cytoplasmic microtubules in inte
mitotic kinetochores in metaphase and spindle midzone
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SIMILARITY: BI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBFAMILY.
PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    requires a license agreement
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    Last sequence update)
    Last annotation update)

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PROSITE; PS50067; KII
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PS50067; KINESIN MOTOR DOMAIN2;
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PS2732; Q15716;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Kinesin-like protein KIPI1 (Kinesin-related motor protein
(Kinesin-like spindle protein HKSP) (Thyroid receptor inte
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore
"Two classes of proteins dependent on either the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead C.M., Rattner J.B.; "Expanding the role of HsEg5 within phases of the cell cycle."; J. Cell Sci. 111:2551-2561(1998).
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MEDLINE=96128120; PubMed=8548803;
Blangy A., Lane H.A., D'Herin P., Harp
"Phosphorylation by p34cdc2 regulates
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                                                                                                                                                                                                                                               EARLY PROPHASE)
SIMILARITY: BELK
SUBFAMILY.
                                                                                                                                                                                                                                                                                                              FUNCTION: MOTOR PROTEIN REQUIRED FOR ESTABLISHING A BIPOLAR SPINDLE. BLOCKING OF EGS PREVENTS CENTROSOME MIGRATION AND J CELLS IN MITOSIS WITH MONOASTRAL MICROTUBULE ARRAYS. SUBUNIT: INTERACTS WITH THE THYROID HORMONE RECEPTOR IN THE PRESENCE OF THYROID HORMONE.

PRESENCE OF THYROID HORMONE.

PTM: PHOSPHORYLATED EXCLUSIVELY ON SERINE DURING S PHASE, BURTH SERINE AND THR-927 DURING MITOSIS, SO CONTROLLING THE ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (PROBABLY DURING ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS APPARATUS (PROBABLY DURING APPARATUS (PROBABLY DURING APPARATUS APPARATUS (PROBABLY DURING APPARATUS APPARATUS (PROBABLY DURING APPARATUS APPARATUS APPARATUS APPARATUS (PROBABLY DURING APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS APPARATUS A
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GO; GO:0005819; C:spindle; TAS.
GO:0004002; F:adenosinetriphosphatase activity;
GO; GO:0003777; F:microtubule motor activity; TAS.
GO; GO:0003777; F:mitotic spindle assembly; TAS.
GO; GO:0007052; P:mitotic spindle assembly; TAS.
InterPro; IPR001752; kinesin_motor.
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EMBL; L40372; AAC41739.1;
PIR; G02157; G02157.
PDB; 1II6; 18-JUL-01.
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                                                    NIMINHMINNNINNIN--VNNNNNNNNNNNNNNNHHHLPQPNYAFTD--TSDFSSLDDMN
                                                                                                    TTQKHLQETKLQLVKEEYITSALESTEEKLHDAASKLLNTVEETTKDVSGLHSKLDRKKA
                                                                                                                                                                                                 FRVMSGKLTVQEEQIVELIEKIGAVEEELNRVTELF - - MDNKNELDQCKSDLQNKTQELE
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ilarity 20.9%;
Conservative 16
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COLLED COLL (POTENTIAL).

COLLED COLL (POTENTIAL).

COLLED COLL (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

PHOSPHORYLATION (BY CDC2).

T-A: NO MITOTIC PHOSPHORYLATION. N
BINDING TO SPINDLE APPARATUS.

RNS -> EL (IN REF. 2).

RW; E322F2141BEF1601 CRC64;
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Pred. No. 9.1e-13
1; Mismatches 38
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RNVSNMNGNVLLGLNKNTHHD----

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KINH MOUSE STANDARD; PRT; 963 AA. 061768; O08771; Q61580; O1-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Kinesin heavy chain (Ubiquitous kinesin heavy KIFSB OR KMS1 OR KHCS.
                                                                                                                                                                                                               MEDLINE=94224818; PubMed=8170981;
Gudkov A.V., Kazarov A.R., Thimmapaya R.,
                                                                                                                                                                                                                                                                                    Meng Y.X., Wilson G.W., Avery M.C., Varden C.H., Balczon R. "Suppression of the expression of a pancreatic beta-cell fo kinesin heavy chain by antisense oligonucleotides inhibits secretion from primary cultures of mouse beta-cells."; Endocrinology 138:1979-1987(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
                                                                                          C. Natl. Acad. Sci. U.S.A. 91:3744-3748 (1994).
FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT. MAY BE INVOLVED IN THE MECHANISMS OF GROWTH ARREST INDUCED BY EXPOSUIDNA-DAMAGING DRUGS OR BY CELLULAR SENESCENCE.
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

MOTOR DOMAIN2; 1.

MOTOR DOMAIN2; 1.

MOTOR DOMAIN2; 1.

KINESIN-MOTOR (BY SIMILARITY).

DOMAIN 329 914 COLL.
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or send a
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
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European Bioinformatics Institute. There a
by non-profit institutions as long as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; L27153; AAA20133.1; -.; L29223; AAA20132.2; -.; P33176; 1BG2.
MGI:1098268; Kif5b.
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               LVDLAGSEKVSKTGAEG-AVLDEAKNINKSLSALGNVISALAEGSTYVPYRDSKMTRILQ
                                       FIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLR
                                                                                                                                               QYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEV-VVKDL
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                                                                                                                       Q----DIFNYIYSMDENLEFHIKVSYFEIYLDKIRDLLDVSKTNLSVHEDKNRVPYVKGC
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AAA20133.1; -.
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21.3%;
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RESULT KINH\_MC

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SDVQIRYV-----

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SEQUENCE OF

1-881 FROM N.A.

TISSUE=Pancreas;
MEDLINE=97266654; PubMed=9112396;

SEQUENCE FROM N.A. NCBI\_TaxID=10090;

suppressor elements: cell immortalization

immortalization.";

DNA-DAMAGING DRUGS SUBUNIT: OLIGOMER CHAINS.

COMPOSED OF

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Roninson I.B.;

"Cloning mammalian genes by expression

in no way

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Q15058;
28-FEB-2003
            TISSUE-Bone marrow;
MEDLINE=96051398; PubMed=7584044;
Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Saki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;
Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human
The coding sequences of 40 new genes (KIAA0041-KIA40080) of analysis of cDNA clones from human cell line KG-1.";
DNA Res. 1:223-229(1994).
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                             Kinesin-like protein
KIF14 OR KIAA0042.
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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28-FEB-2003
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(Rel. 41, Last annotation update)
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1
Motor_protein; Microtubules; ATP-binding;
DOMAIN 355 628
KINESIN-MOTOR
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InterPro; IPR001752; kinesin_
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                                                                                                    KKGLINYKSTLYNDNTINKKHNNNNNNNNNDNNDNNNNNNNNNDSSSMVNNMINHMINN
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Pred. No. 1.7e-12;
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                   NNHLPQPNYAFTDTSDFSSLDDMNCHLN
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Mouse)
    Mus musculus (Mouse
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHFLENGNNKAASVQEEFMDAVCDGVGLGMKILLDSGLEKAKELQHELFRQCTKNEVTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHFKEKYTYPTLSTNEDIYNKEME----GKHIRLDD-QDKYDDNDNNNVDNNNKNNVDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLEDELRQEVKKLGGYLQLFLQGCCLDISSMIKEAQKNAIQIVQQAVKYVGQLAVLKGSK 1395
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                                                                                                                 (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 36, Last annotation update)
protein KIF3A (Microtubule plus
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                                                                                                                                                                                                                                     STANDARD;
Chordata;
Rodentia;
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    Craniata; Vertebrata; I
Sciurognathi; Muridae;
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    Euteleostomi; 
; Murinae; Mus
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Best Local Sim
Matches 145;
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PROSITE; PS0041; KINESIN MOTOR DOMAIN; 1.

PRÓSITE; PS50067; KINESIN MOTOR DOMAIN; 1.

PRÓSITE; PS50067; KINESIN MOTOR DOMAIN; 1.

MOTOR DOMAIN; 1.

350

KINESIN-MOTOR (BY SIMILARITY).

DOMAIN

351

586

COLLED COLL (BY SIMILARITY).

GLORITLAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUB
ACTIVITY IN VITRO.

-!- SUBUNIT: HETERODINER OF KIF3A AND KIF3B.
-!- TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY
-!- TISSUE (MAINLY IN THE CEREBELLAR GRANULAR LAYER)

TYPE OF NEURONAL CELL.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN F
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"Kinesin family in murine central nervous
J. Cell Biol. 119:1287-1296(1992).
-!- FUNCTION: MICROTULLE-BASE
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InterPro; IPR001752; kinesin_motor.
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HSSP; P17119; 3KAR.
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                          KLTRLLQDSLGGNSKTMMCANIGPADYNYDETISTLRYANRAKNIKNKAR-INEDPKDAL
                                                                   ELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEED----
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Pred. No. 7.1e
84; Mismatches
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POLY-ARG.
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TEC P38738; O9Z2F8;

TEC P1992 (Rel. 24, Created)

TEC 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/c;
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                                                                                      EMBL; AF067180;
HSSP; P56536; 2
                                                                                                                          EMBL; X61435; CAA43677.1;
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?; P5655; American problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the problem in the pr
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TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY
KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRA
ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CI
DIMERIZATION; AND A SWALL GLOBULAR C-TERMINAL DOMAIN WHICH
INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CI
VESICLES AND MEMBRANOUS ORGANELLES.
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                                                                                                                                                                                                                                                                                                                   SEQUENCE.
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Sciurognathi; Muridae;
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kinesin
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Best Local (
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NP_BIND
SEQUENCE
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOR_DOMAIN2; 1.

MICROCLUBULE; ATF-binding; Coiled DOMAIN

1 386
KINESIN-MOTOR (BY S: DOMAIN 406 923 COILED COIL.
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PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISc; 1.
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                                          741
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Pred. No. 1.2e
62; Mismatches
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N; D5A8C701A2911AB2
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Q91784; Q9PSIO;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
28-FEB-2003 (Rel
                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restr
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               Vernos I., Heasman J., Wylle C.;
"Multiple kinesin-like transcripts in Xenopus oocytes.";
Dev. Biol. 157:232-239(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spindle organization and Cell 81:117-127(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95236444; PubMed=7720067;
Vernos I., Raats J., Hirano T., Heasman J., Karsenti E.,
"Xkipi, a chromosomal Xenopus kinesin-like protein essent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
Chromosome-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XENLA
                                                                                                             InterPro; IPR001752; kinesin_motor
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                  EMBL; X82012; CAA57539.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 9-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                     Motor protein; Microtubules;
Nuclear protein; Coiled coil.
                                                              PROSITE; PS00411; KINESIN MOTOR DOMAIN1; PROSITE; PS50067; KINESIN MOTOR DOMAIN2;
                                                                                                                                       HSSP; P17119; 3KAR.
                                                                                                                                                   PIR; I51617; I51617.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93246065;
                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                              FUNCTION: REQUIRED FOR MITOTIC SPINDLE STABILIZATION. SUBCELLULAR LOCATION: NUCLEAR, CHROMOSOMES.
                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO T
CHROMOKINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                          BRAIN. . SIMILARITY:
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1007
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PubMed=8482413;
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1006
1226
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                                                                                                                                                                                                                              institutions as long as
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Last annotation update)
kinesin KLP1 (Chromokinesin)
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KINESIN-MOTOR.
COILED COIL (E
GLOBULAR.
                                                 ATP-binding; DNA-binding;
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Best Local
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                                                                                                                                                 EG52_XEI
Q91783;
                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Kinesin-related motor protein Eg5 2.
Renopus laevis (African clawed frog).
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CONFLICT
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                                                                                                                                                                                                                                                                                                   IKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELQRLKLQVQELQVLLLQAHGGTL---PVLNSMEPSENLQSLMERNK-NLEKENGKLSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTERIS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-GKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAM-DSDK--NHIPFR
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Pred. No. 1.8
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I -> L (IN REF. 2).
WW; 7F0275FCF3316697
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SEQUENCE FROM N.A.

NCBI\_TaxID=8355; Xenopodinae; Amphibia; Batrachia;

Xenopus

TISSUE=Egg;

Eukaryota;

Metazoa; Chordata;

Anura;

Mesobatrachia;

Craniata; Vertebrata; Euteleostomi; esobatrachia; Pipoidea; Pipidae;

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Best Local S
Matches 198
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Dev. Bio
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NP_BIND
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                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMUULZ; ALEV, SIN MOTOR DOMAIN1; 1
PROSITE; PS50041; KINESIN MOTOR DOMAIN2; 1
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X71864; CAA50695.1; PIR; I51616; S33417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: CONCENTRATED AROUND THE POLAR ENDS O
BOTH MEIOTIC AND MITOTIC SPINDLES.
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN UNFERTILIZED EGGS,
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN UNFERTILIZED EGGS,
-ESPECIALLY IN THE GERMINAL VESICLE AND IN THE RADIAL YOLK-
CHANNELS. ALSO PRESENT IN TESTIS:
-i- DEVELOPMENTAL STAGE: ACCUMULATES DURING THE LATTER STAGES
OGGENESIS AND LEVELS INCREASE THREE-FOLD DURING OOCYTE MAT
LEVELS DECREASE AFTER FERTILIZATION.
-i- PTM: PHOSPHORYLATION DURING MITOSIS AT THR-937 CONTROLS TH
ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (BY SIMILARI
-I- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :-
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DOMAIN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00225; kinesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00380;
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long
                                                                                                                         YIERHEFIVDKVFDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS
                                                                                                                                                                                      MNSK-----
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  DVGERLQMFDDPRNKRGV1 I KGLEE1 SVHNKDEVYQ1 LERGAAKRKTASTLMNAYSSRSH
                         ---KRKMVAALENGKKEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSH
                                                   RSSDEEFTWEQDPLAGIIPRTLHQIFEKLS--EIGTEFSVKVSLLEIYNEELFDLLSPSP
                                                                            Q-----PYGQSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQ---
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692
884
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937
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22.1%;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
PHOSPHORYLATION (BY CDC2) (BY
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                                                                                                                                                                                                                        Score 439.5; DB Pred. No. 2e-12;
                                                                                                                                                                                                                                                                             SIMILARITY
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2; 1.
ng; Coiled coil; Mitosis;
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                                                                                                                                   MEDIINE=98290545; PubMed=9628581;
Nagase T., Ishikawa K.-I., Miyajima N.,
Nomura N., Ohara O.;
"Prediction of the coding sequences of
The complete sequences of 100 new cDNA
code for large proteins in vitro.";
DNA Res. 5:31-39(1998).
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Best Local Sin
Matches 216;
                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   DOMAIN
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                      PROSTTE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KIRESIN_MOTOR_DOMAIN2; 1.
PROSITE; PS50067; KIRESIN_MOTOR_DOMAIN2; 1.
Motor_protein; Microtubules; ATP-binding; Coiled_DOMAIN 1 386 KINESIN-MOTOR (BY SIDOMAIN 406 923 COILED_COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005871; C:kinesin complex; TAS.
GO; GO:0003777; F:microtubule motor activity; TAS.
GO; GO:0006996; P:organelle organization and biogenesis;
InterPro; IPR001752; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunit of dynactin.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1997) to A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00225; kinesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF010146;
HSSP; P56536; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAINS.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN,
TESTIS, AND MODERATE EXPRESSION IN KIDNEY, SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N
TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF
KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL
ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN
DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VESICLES AND MEMBRANOUS ORGANELLES.
SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00380; KINESINHEAVY.
                       ERFVSSPEEVMDVIDEGKANRHVAVTNMNEHSSRSHSIFLINIKQENVETEKKLSGKLYL
                                      ILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTS---LGKIAF
                                                                        RIAHDIFDHIYSMDENLEFHIKVSYFEIYLDKIRDLLDVSKTNLAVHEDKNRVPYVKGCT
                                                                                                 YAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEV-VVKDLK
                                                                                                                          NTTQEQVYNACAKQIVKDVLEGYNGTI---FAYGQTSSGKTHTMEGK--LHDPQLMGIIP 110
                                                                                                                                                  TVDNFTVYENTIKPLIIDLYE--NGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQ 121
IDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAM-DSDKNHIPFRDSELTKVLR
                                                                                                                                                                                                    IKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYI-ERHEFIVDKVFDD
                                                                                                                                                                           IKVMCRFRPLNEAEILRGDKFI-------PKFKGDETVVIGQGKPYVFDRVLPP
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MICROTUBULE-BINDING.

ATP (BY SIMILARITY).

TLKNVI -> STHASV (IN R

EFT -> DRV (IN REF. 2)
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Pred. No. 1.9e-12;
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                                       VNNNMGNINIS - - - -
                                                                                                                         SMNFCHYNLIDKNYLIDLNNKEOKDKNIHGCDNNIIONRNDFEKKKKTNFYNNN--NIVI
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                                       PRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKD
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KINH DROME STANDARD; PKT; y 17120; Q9V7L9; C1-AUG-1990 (Rel. 15, Created) 16-OCT-2001 (Rel. 40, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation
SEQUENCE FROM N.A.

MEDLINE=89168428; PubMed=2522352;

Yang J.T., Laymon R.A., Goldstein L.S.B.;

"A three-domain structure of kinesin heav-
sequence and microtubule binding analyses

Cell 56:879-889(1989).
                                                                                                                                                                                   Kinesin heavy chain.

KHC OR KIN OR CG7765.

Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo.

Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,

Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                  _TaxID=7227;
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analyses."
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hy, Hoskins R.A., Galle R.F.,
RA Bananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Banton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Batton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Batton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Beyaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Helman T.J., Wein M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Worris J., Woshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., McPherson D.R.,
RA Melson D.R., Nelson K.A., Stapleton M., Strong R., Sun B.,
RA Spier E., Sjradling A.C., Stapleton M., Strong R., Sun B.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Spier E., Zaveri J.S., Zhan M., Jang G., Zhou X., Smith H.O.,
RA Spier S. H., Rubin G.M., Zhang G., Zhou X., Smith H.O.,
RA Spier S. H., Rubin G.M., Zhang G., Zhou X., Smith H.O.,

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SEQUENCE FROM N.A.
STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                        -I- DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE WOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL ALPHA-RELICAL COLLED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS), VESICLES AND MEMBRANOUS ORGANIELLES.

-I- MISCELLANBOUS: MUTANT FILES DISPLAY IMPAIRED ACTION POTENTIAL PROPAGATION AND NEUROTRANSMITTER RELEASE AT NEUROMUSCULAR JUNCTIONS, BUT ARE STILL CAPABLE OF TRANSPORTING CERTAIN MEMBRANES, INCLUDING SYNAPTIC VESICLES, TO THE NERVE TERMINAL.

-I- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN SUBFAMILY.
use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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879 RCELPKLEKRLRCTMERVKALETALKEAKEGAMRD 913	879 RC	Db
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A;Cross-references: C;Genetics:

EMBL: Z98547; NID: e1325376; PID: e1325396; PIDN: CAB11121.1

A;Note:

C0425w

Query Match Best Local Similarity

11.5%; 21.0%;

Score 789.5; DB 2; Pred. No. 2.7e-25;

Length 4550; Indels 683;

Matches 380;

Conservative

247;

Mismatches

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Gaps

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A; Map position: 3

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256 TOTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKSKSIMIANISPTI 315

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955 NLNILKLI----KEKIIQVLQNNYKQVCVFCKKTTGIKTKCMFPSCSTYFHIYCYYNKYM

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69 TVYENTIKPL----IIDLYENGCV------CSCFAYGQ--TGSGKTYTM-----L

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RESULT 1 T18440 Hypothetical protein C0425w - malaria C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revisio C;Accession: T18440 R;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, AA;Reference number: Z18935 A;Recession: T18440 A;Retatus: preliminary; translated from A;Residues: 1-4550 <law>A;Residues: 1-4550 <lawaa;a;residues: 1-4550="" <lawaa;a;a;a;a;a;a;a;a;a;a;a;a;a;a;a;a;a;<="" <lawaa;a;residues:="" th=""><th></th><th>52</th><th>44 529.5</th><th></th><th>42 533</th><th>41 533.5</th><th>40 534</th><th>39 534.5</th><th>38 537.5</th><th>36 541.5</th><th>35 542.5</th><th>34 543</th><th>33 544</th><th>32 549</th><th>31 552</th><th>30 560.5</th><th></th></lawaa;a;residues:></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law></law>		52	44 529.5		42 533	41 533.5	40 534	39 534.5	38 537.5	36 541.5	35 542.5	34 543	33 544	32 549	31 552	30 560.5	
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(Plasmodium falciparum) 999 #text_change 09-Jun-2000 DDBJ		hypothetical prote	asparagine-rich pr	kinesin-like prote	trfA protein - sli	carbamoyl-phosphat	kinesin-related pr	RAD2 endonuclease	ser/Thr protein ki	kinesin-related pr	hypothetical prote	P-type cation tran			hypothetical prote	DNA-directed RNA p	

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C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18499
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18499
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Introns: 87/3
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                                              HMDI-LQKYDHDYFSLSENIKKEISQCKINIPHISDEAKQKMPAIIGVYNTNGLKKEKQS
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-NRSSCDNIMNKKKNNLH-LARHSVGSKLTMFSYD--
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mitotic centromere-assocated kinesin MCAK [imported] (Species: Leishmania major (C;Species: Leishmania major (C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #t (Accession: C81455; T02791 C;Accession: C81455; T02791 L; deVos, T.; Hixson, G.; F
                                                                                                                                                                           RESULT 4
T02791
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
C;Dates: 261455; T02791
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: C81455
A;Status: preliminary
A;Molecule type: DNA
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    Leishmania major (strain

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A;Note: MCAK
C;Superfamily: k:
F;135-459/Domain
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Best Local
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                                                  RHEFIVDKV-----FDDTVDNFTVYENTIKPLIDLYENGCVCSCFAYGQTGSGKTYT
                                                                                                                SELEKK-----
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A;Residues: 1-668 <PYL>
A;Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24615.1;
A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
C;Genetics:
A;Gene: MCAK
                                                                                                                                                                                                                                                                            R;Lawson, D.; Bowman, S.; Barrell,
submitted to the EMBL Data Library
A;Reference number: Z18935
A;Accession: T18501
A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C0760c - malaria [C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision C;Accession: T18501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: kinesin-related protein KIF2; kinesin motor; 135-459/Domain: kinesin motor domain homology <KMOT>
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                                                                              Score 752; DB 2; I
Pred. No. 7.4e-24;
9; Mismatches 432;
                                                                                                                                                                                                                         NID:e1331903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 755; DB 2; L
Pred. No. 9.8e-25;
7; Mismatches 134;
                                                                                                                                                                                                                                                                                    from
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                                                                                                                                                                                                                                                                                                                                             August
                                      ---KKDSDIITVKNNCTLYIDE----PRYKVDMTKYIE
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                                                                                                                                                                                                                                                                                  GB/EMBL/DDBJ
                                                                                                                                                                                                                           PID:e1331922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Plasmodium falciparum)
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                                                                                                                    Length 3394;
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                                                                                416;
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1083 NNNEYLSYFQKNVDTIINNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVIKKYINED 1142	1023 DKYDDNDNNNVDNNNKANVDNNVDNNVDNNVDNNVDNNVDNNVDNDDDDVDFHNIKNF 1082	974 IIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQ 1022 :: ::::       :   :   :   :   :   :   :	925 SSSSSNINIYNNINDDTFQNDYCHNDNTFTIRKKNİTNINSNIYQNDD 973 :   :   :     :     :	865 NNIVIVNNNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSS 924 :	814 NFCHYNLNDKNYLIDLNNKEQKDKNIHGCDNNIIQNRNDFEKKKKTNFYNN 864	755 NNNIDVENYNNRDGTNNSMKLYAYNSHNLFQPDNNKNTSNIQNI-NTNKNNQDGNVNYSM 813    ::	695 KSNYNSNQSISDVQIRYVNEMDTSNKNIDNIFFDAISCDNIMYPNITININININININININ 754	635 VLLGLNKNTHHDISTKDENHNDNKINNGVINIINNSNVNSINNSNVNSINNSNVNSISTY 694	580 HLARHSVGSKLTMFSYDDQKNKDNTFFKSNINKM-EDNTFKDILYESRNVSNMNGN 634	
Qy 518 HLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIF-LHKKNLRDNIKLKN 564	Qy 458 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Qy 403NKSFDKPREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYNDNTINKKHNNN 457	Qy 347 TNTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILK 402	Qy 287 RDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDD 346 :	Qy 227 NKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPF 286	Qy 181ILRVLTKEELILKMIDGVLLRK-IGVNSQNDESSRSHAILNIDLKDI 226 	Qy 134 YDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK 180 	Qy 79 IIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYAAGDIFTFLNI 133	Query Match 10.9%; Score 748.5; DB 2; Length 1817; Best Local Similarity 23.6%; Pred. No. 5.3e-24; Matches 356; Conservative 197; Mismatches 410; Indels 543; Gaps 69;	1143 IKNMSLEBIDKTANGSIYEKRKVLLTKLLLFKKNVDTQINN  1143 IKNMSLEBIDKTANGSIYEKRKVLLTKLLLFKKNVDTQINN

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|: :::| | |: |: | :| |: |: |
LYILYIIRKKQYEHVKSILYDKSNENYFRFNENKDIKMENTNMLYNIILNNFSTEDHDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CISLYNSISLYSNKNTSFNHLYNNIYDTCFIQNNYISNQQVQNYKNEKNTNMEHYNEKKL
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                                                    NNKHNN
                                                                                      SMDHNN
                                                                                                                        LLNIQWNYIFPMDLFISSNLSHETELIINKLEQNILNNNNNNNN---
                                                                                                                                                            FLVVEYQ---
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                                                                                                                                                                                                                               ETSDLRKDLVMCHICNNNPDDQFHFYAYSRLEKDIINLIMLRQIWCE----SENLRLLYQ
                                                                                                                                                                                                                                                                                                                                             KNLFCYTNHLSLLYF----
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R;deHostos, E.L.; McCaffrey, submitted to the EMBL Data L: submitted to the manual L: A;Reference number: Z18853
A;Accession: T18277
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Kinesin heavy chain - slime mold (Dictyostelium discoideum)

C;Species: Dictyostelium discoideum

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_ch

C;Accession: T18277
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A;Molecule type: mRNA
A;Residues: 1-1254 <DEH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIFGYQETQSQIFEDVAEPIVND-FLDGYHGTIIAYGQTASGKTFTMV---
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 NDNNSNSGGLRVSTSYITSSPNLSIKEYGCH---HNSPPLFSYFKTKDFPPSSDENDKFF
                                                                                                     NSIYKSNYNSNOSISDVQIRYVNEMDTSNKNNDNIFFDAISCDNNMYPNITNNNNNNNNN
                                                                                                                                                                             WNGNVLLGLNKNTHHDISTKDENHNDNKINNGVINIINNSNVNSINNSNVNSINNSNVNS
                                                                                                                                                                                                                                                                                                                          {\tt NNNSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSSCDN}
                                                                                                                                                                                                                                                                                                                                                                                                                                   QKLELLNSQISSNHSFD------NTFKEIENTCENSK-----IIFDD--L
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                                     NNNNN-----
                                                                       ----SDGYLNRSLKDIKIPEISDLNDHNINN
                                                                                                                                               IILNSTLG
                                                                                                                                                                                                                                                  IMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKMEDNTPKDILYESRNVSN
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ilarity 22.3%;
Conservative 21
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                                                                                                                                               --NISDDDDDDDDHHSNN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7%; Score 732; DB 2;
3%; Pred. No. 1.7e-23;
217; Mismatches 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                     - NIDVENYNNRDGTNNSMKLYAYNSHNLFQPDNNKNT - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1254;
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                                                                                                                                                                                                                        KVEDLRDLD---DEPDIED
                                                                                                                                                -NNVDDNNNGEINND----
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                                                                             NINNNNIN
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A44259

kinesin-related protein KIF2 - mouse
c;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994
C;Accession: A44259; S27871
R;Aizawa, H; Sekine, Y; Takemura, R; Zhang, Z;
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous
A;Reference number: A44259; MUID:93077686; PMID:1
                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:D12644; NID:g220467; PIDN:BAA02165.1; PID:g220468
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-716 < AIZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A44259
                                                                                                                                                                                                                                                 Superfamily: kinesin-related protein KIF2; kinesin motor domain; Keywords: ATP; microtubule binding; nucleotide binding; P-loop; 196-531/Domain: kinesin motor domain homology <KMOT>, 285-292/Region: nucleotide-binding motif A (P-loop); 291/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                          Similarity
                                                                            KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
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TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY
                                               RICVCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYLENQTFRFDYAFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDKTAQSIYE------KRKVLLTKLL-------LLFKKNVD-TQINNETSDLRK 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IFGSAIDLRFSGDDVINSIECKRAIHKLKTNNYVNGDLDQQQQQHNY--ITKIDQLSEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDNNNVDNNVCNNDK-NNVD------NNNVDND-DDDVDFHNIKNFNNNEYLSYFQ 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIYSDYPTNEKISLAQHNQISLAKELYGGNSKQYYDEMSSFNTAYNHLIEMNHLETAVSK 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --YPTLSTNEDI----YN-----KEMEGKHIR--LDDQDKYDDNDNNNVDNNNKNNVDNN 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSPSSSTTTSIKKKNFNKRRSWIIFTIILTITLVSSSLLCLYLPEYKERLVQRRGYLNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSIFNKNGNITIKEFETPQQQQQQQQQQQQQQQQQQQQQQPLILQTTSTNPTIISIKSNKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNEMKNNEMKDNEMKDNHIKSNNNNSSSSSSSNNNIYNNINDDDTFQNDYCHND----NT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDKTITSTIERETIQPSSLSNSTSLLDIETVESSTLPAPPPVTTTTTTTTTTTTKLTKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EKGGEKVLEDQIISLRNDKNTLSTQILNLEGDKKSLGVLVIKLNSDKTEIQNEVKELKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEQNQLIENF -- KLDLK---NKTSEIEK---LEKEIKQKDNKIKEKEEKIELIESRVLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNVDTIINNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVIKKYIN--EDIKNMSLEE 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SNIQNINTNKNNQDGN------VNYSMNFCH----
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                                                                                                                                                                          10.6%;
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                                                                                                                                                                          Score 728; DB 1; Length 716; Pred. No. 1.4e-23;
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-Mar-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system; PMID:1447303
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                                                                                                                                                  Indels
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F;205-542/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene; KRP2
C;Superfamily: kinesin-related protein KIP2; kinesin m
C;Superfamily: kinesin motor domain homology <KMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinesin-related protein 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16
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A; Residues: 1-671 <SP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, January A;Reference number: Z17121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T
R; Sperry, A.O.
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A;Experimental source: strain Sprague-Dawley, testes
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                                                 550 TEEMDASS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
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71; Conservative
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                                                                                                 GSEMNASSIENVVIKSNHLLSNNNNNKIN--RGKINDKIERNNILKNKSFDKPRE
                                                                                                                                                                                  VGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSK
                                                                                                                                                                                                                                                 LAGNERGADTSSADROTRMEGAEINKSLLALKESIRALGONKAHTPFRESKLTOVLRDSF
                                                                                                                                                                                                                                                                           LAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIF
                                                                                                                                                                                                                                                                                                                                                  EYLVTCADD-VIKMINMGSACRTSGQTFANSNSSRSHACFQILLR--AKGRLHGKFSLVD
                                                                                                                                                                                                                                                                                                                                                                                 ASRDVFLLKNQPRYRSLNLE-VYVTFFEIYNGKVFELLNKKAKLRVLEDSKQQVQVVGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGDIFTFLN--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDLAGNERGADTSSADRQTRLEGAEINKSLLRLKECIRALGRNKPHTPFRASKLTQVLRD
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Pred. No. 2.3e-23;
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A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: D71618
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;Residues: 1-1436 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ypothetical protein PFB0285c - malaria parasite (Plasmodium falciparum);Species: Plasmodium falciparum
;Species: Plasmodium falciparum
;Date: 13.Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2
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Matches 354; Conserv
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Cross-references: CB:AE001385;
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Pred. No. 5.3e-22;
                                 -SMPNMSTTSSMNMSGLNTSSSEGLTNIINMNNINSVNN--
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Sutton, G.G.; Clayton,
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A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: B71605 hypothetical protein PFB0850c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; (
.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, 
Science 282, 1126-1132, 1998 C:Accession: A; Experimental source: A;Residues: 1-807 A; Molecule type: DNA A;Status: preliminary; nucleic acid sequence A; Cross-references: B71605 <GAR> GB:AE001420; ce: clone 3D7 GB:AE001362; not shown; Cummings, L.M.; , G.G.; Clayton, NID: g3845287; translation PIDN:AAC71959.1; PID:g38452 Aravind, L.; Koonin, R.; White, O.; Smith not shown Smith,

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Best Local Similarity
Matches 242; Conserv
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A;Map position: 6
C;Superfamily: response regulator homology
C;Keywords: autophosphorylation; phosphoprotein; phosphotransferase;
F;2027-2142/Domain: response regulator homology <RRH>
F;2076/Binding site: phosphate (Asp) (covalent) #status predicted
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R;Wang, N.; Shaulsky, G.; Escalante, R.; Lo
EMBO J. 15, 3890-3898, 1996
A;Title: A two-component histidine kinase (
A;Reference number: $71629; MUID:96324397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-2150 <WAN>
A;Cross-references: EMBL:U42597
A;Experimental source: strain A
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                                            RTKGNHS---KTNSLQDFETS-----
                                                                                                                                                              HIKSNNNNSSSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQ----
                                                                                                                                                                                                                      SSNNNNQSNNNTNPSINNNNGRN---
                                                                                                                                                                                                                                                         KKKKTNFYNNNNI VI VNNNMGNNNSPRMKYGL/CGSHTS I DNMKNNEMKNNEMKDNEMKDN
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                                                                                   -NDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYD
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146;
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Pred. No. 6.8e-21;
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                                            -SMNGGDDSISGAGSGGSLRRRNKDDND
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hypothetical protein K11D9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to C;Accession: T23607
R;Wall, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A;Reference number: Z19769
A;Accession: T23607
A;Status: preliminary; translated f
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A;Cross-references: EMBL:Z92807; PIDN:CAB07264.1; GSPDB:GN00021; CESP:K11D9.1
A;Experimental source: clone K11D9
C;Genetics:
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                                                                                                                                                                                   DLAGNERGQDTRECDRDTRKEGANINTSLLALKECIRGMARNSSHVPFRQSKLTMVLRDS
                                                                                                                                                                                                                                                                                                                      LTARDVFRMLEQPQYRRKD--LSVHCAFFEIYGTKTYDLLNDKAELRVLEDKMQKVQVVG
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                                                  KSDEEYDEMVEKQEHRRVAVDHVRNLKDMSEKIIRETTIVLSNEPSAAQKAECLAKLDQ
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                                                                                  TNTERISILDSKGSE--
                                                                                                                   FIGEKSRTVMISMISPGISSSDHTLNTLRYADRVKEMGTDGSGEATPIRDEELFLPPSAD
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Pred. No. 1.4e-20;
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C;Species: Plasmodium falciparum
C;Date: 20-Feb-1995 #sequence_revision 20
C;Accession: S14556; S14548
R;Schreiber, L.; Deutsche, U.; Storck, T.
submitted to the EMBL Data Library, Decem
A;Reference number: S14469
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A;Residues: 'Q', 210-1251,'NEENDETALDTIIQPPIKKKK' <SC2>
A;Cross-references: EMBL:X17488; NID:99852; PID:99853
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A;Status: preliminary
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A;Molecule type: mRNA
A;Residues: 1-1256 <SCH>
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llarity 22.1%;
Conservative 14
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Library, December 1989
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Pred. No. 6.9e-20;
9; Mismatches 341
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A;Cross-references:
C;Genetics:
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A;Accession: T18429
A;Status: preliminary; translated
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C0345w - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_chC;Accession: T18429
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Best Local Similarity
Matches 284; Conser
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                                              LTEYNDKKDLV-GYWLLSQNNEKDMKELYHILCAIKKKNPKAARIPSFYPKINMNNSMFN
                                                                                                                              NNLSNDIESIICLSNV-----EIKMF
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                                                                                      MNASSIENVVIKSNHLLSNNNNN-----
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Conservative 202;
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Pred. No. 2.8e-18;
02; Mismatches 406;
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v, August
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      -GKY--SSLNDIDKIKKNKKKGLINY
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                                                                                                                              -NDPNITNITILEKRNYSYGIE
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hypothetical protein C0485w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan C;Accession: T18477 R;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, November 1998 A;Reference number: Z18937 A;Reference number: Z18937 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-2523 <LAM>
                                                                                                                                                                                                                             RESULT 16
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                                                                                                                                                                                                                                                                                                             DLKKIQEQVERKIRKYKIQMDQENKKPPPSKNKINMKSINLDIDDDQNVDSQ
                                                                                                                                                                                                                                                                                                                                                   D-NVIKKYINEDIKNMSLEEIDKTAQSIYEKRKVLLTKLLLLF--KKNVDTQ 1180
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                                                                          ------NVNSINN-SHMMSINNSNMSIYKSNYNSNQS--ISDVQIRYVNEMD
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                                 TSNKNNDNI FFDAISCDNNMYPN--ITN----NNNNNNNNNNNNNNNNI DVENYNNRDGTN
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                                                                                                                                                                                                                                         INYKGPATKALVNKLFISKKESKRAIT----SSKKRDD----DNINVIKKINTPSOKVS 1509
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Query Best I Match Qy	RESULT T18489 hypothet C;Specil C;Date: C;Acces R;Lawses R;Lawses R;Estatu A;Molect A;Resid A;Cross C;Genet A;Map p A;Map p	Q9 Q9	Db \$	OV DB	Qy	g 49	B &	ОУ	od VQ	Db Qy	D QY	ОУ	Db Qy	DD QY
8.8%; Score 601.5; DB 2; Length 4981; st Local Similarity 20.3%; Pred. No. 2.1e-17; ches 313; Conservative 256; Mismatches 457; Indels 519; Gaps 75; 17 LEKKKKDSDITTVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD 63	RESULT 17  T18489  T1849  hypothetical protein C0820w - malaria parasite (Plasmodium falciparum)  C; Species: Plasmodium falciparum  C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000  C; Accession: T18489  R; Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, August 1997  A; Reference number: Z18935  A; Accession: T18489  A; Racession: T18489  A; Rosidues: preliminary; translated from GB/EMBL/DDBJ  A; Molecule type: DNA  A; Rosidues: 1-4981 < LAW> A; CGenetics: A; Map position: 3  A; Note: C0820w	1268 NKKLVQDNIKNSMDHNNIHKK 1288 	: : : 203 KKNIVKFKSVENRTPHTYLLFKNDENKAYLEMVKSVNYMNK	2158LKKNVNVNVNKDIHIINDKHERICTKNNNPNLHICQPTNDQDGDK 2202	TQINNE	1112 YDDTKEILNNILLSKYKAEKDNVIKKYINEDIKNMSLEEIDKTAQSIYEKRKVLL 1166	1052 NAVDNNDKNNVDNNNVDNDDDDVDFHNIKNFNNNEYLSYFQKNVDTIINNCLNSLDISSM 1111	1001 LSTNEDIYNKEMEGKH-IRLDDQDKYDDNDNNIVDNNIKANIVDNNIVDNNIVD 1051	966SNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPT 1000	923 SSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNIN 965   : :	9 0	821 -NDKNYLIDLNNKEQKDKNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIVI 869 	789 NKNTSNIQNINTNKNNQDGNVNYSMNFCHYNL	-SMKLYAYNSHNLFQPDN 7 

782 NLFQPDNNK-NTSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLNNKEQK 835		432 NKKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	230 TS	
105GMNNIIHFKNKYDNNNSSMKNTDNNKLIGLIKNTHH  591 TMFSYDPQKNKDNTFFKSNIIKMEDNTPKDILYESRNVSNWNGNVLIGLIKNTHH	A;Cross-references: GB:M24328; GB:X03716; NID:g160091; PID:g160092  Query Match Best Local Similarity 28.5%; Pred. No. 3.1e-18;  Matches 212; Conservative 92; Mismatches 193; Indels 246; Gaps 39;  Qy 424 NDIDKIKKNKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNDNSSSMV 483   :	RESULT 18 A23770 A23770 asparagine-rich protein - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jun-2000 C;Accession: A23770 R;Stahl, H.D; Bianco, A.E.; Crewther, P.E.; Burkot, T.; Coppel, R.L.; Brown, G.V.; And: Nucleic Acids Res. 14, 3089-3102, 1986 A;Title: An asparagine-rich protein from blood stages of Plasmodium falciparum shares d: A;Reference number: A23770 A;Accession: A23770 A;Accession: A23770 A;Molecule type: mRNA A:Residues: 1-537, SCRA	OY 1110 SMYDDTKELLNULLKYKARKDNVIKKYLNBDIKNMSJEELDKTAGSIYEK 1161	2561 EGCCNKEESGHENNSKGIKNIVSKRGEENMGEKKRNNKRTKYKVQEEK  973 DIIYTINSLNDYMSNTILHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNUNN

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	764 NURDGTUNSMKILYAYUSHNIFQ
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	291 SLNKNKCLTGTIKKEKYMIPKGTEYQDKEKESSILTINQNDKKYKKKKKKYSEL 344  307 MIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSKGSBMNASS 366

Qy 411 EGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYNDNTINKKHNNNN 458	Qy 358 KGSEMNASSIENVVIKSNHLSNNNNNKINRGKINDKIERNNILKNKSFDKPR 410	Qy 311 ISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDS 357	Qy 255 QTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKSKSIMIAN 310	Qy 205 VNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGSERGADTVSQNK 254	QY 191LRXIDGVLLRXIG 204  Db 511 QKHYYSTSNINLLYNNIGKVLDNGLHLSNNMYCRLNSNPPYKSISLINNNVFFYKKRKSN 570	Qy 132 NIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILRVLTKEEL- 190	QY 81 D-LYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYAAGDIFTFL 131	Qy 21 KKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDDTVDNFTVYENTIKPLII 80   :: :   : : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : : :   : : :   : : :   : : :   : : : :   : : :   : : :   : : : :   : : : :   : : : :   : : : :   : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : : :   : : : : :   : : : : :   : : : : : :   : : : : :   : : : : :   : : : : : :   : : : : : : : : :   :	Query Match 8.6%; Score 587; DB 1; Length 2485; Best Local Similarity 20.5%; Pred. No. 4.1e-17; Matches 356; Conservative 249; Mismatches 517; Indels 616; Gaps 85;	A;Gene: PPB0150c C;Superfamily: malaria parasite serine/threonine-specific protein kinase PFB0150c; prote C;Keywords: phosphotransferase F;2087-2352/Domain: protein kinase homology <kin></kin>	A;Residues: 1-2485 <gar> A;Residues: 1-2485 <gar> A;Cross-references: GB:AE001376; GB:AE001362; NID:g3845108; PIDN:AAC71820.1; PID:g384510 A;Experimental source: clone 3D7 C;Genetics:</gar></gar>	A71600; MUID:99021743; PMID:9804551  Y; nucleic acid sequence not shown; translation not	R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; .; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.	threonine-sples: Plasmodines: Plasmodines: 10-Sep-1999; 1	RESULT 20	Qy 1251 NSVLLNVSSNNGDIILLNKKLVQDNIKNSMDHN-NIH 1286	Qy 1203 DDQFHFYAYSRLEKDIINLIML-RQIWCESENLRLLYQFLVVEYQNKSA 1250 ::   :     :     :     :       :	Db 1270 IINDVLKSDDKFENMINSKEINIKDFKCVDKANDICLNLNELNKQSYNSNT 1320
QY 1150 EIDKTAGSIYEKRKVLLTKLLLFKKNVDTQINNET 1185	OY 1117 EILMNI LISKYKAE KONVIKKYINEDIKNMSIE 1149	1058 DKUNVUNUNVUNDU-UDVDEHNIKAPINNESUSTEQKNVOTIINKULNSUDISKYDDYK	1009	1556 HDESPSRDDNCILLKIEGRSKKYSDITLYNEDKSNLENDNETINEYENVCSNIDVNEWE	909 NEMKONHIKSNNNNSSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNI 	QY 858 KTNFYNNNIVIVNNNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKD 908	Db 1390 KLNEKMNISMSNDEDMIPTLNSEHGNUFPSCQPNLLEKKSTYIDLNLYDSNSMDDF-TEE 1448	798 IN'INKUNQUGNUN'SMINECHYNLINDKNYLIDLNUKEQOKU	768GTNNKKLYAYNSHNLFQPDNKNTSNIQN 11.SMLYAYNSH-NLFQPDNKNTSNIQN	Qy 748 NNNNNN 767	Qy 715MDTS-NKNNDNIFFDAISCDNIMYPNITNNNNNN 747	Qy 672VNSINNSNMNSINNSNMNSNSIYKSNYNSNQSISDVQIRYVNE 714	Qy 658 KIN	Qy 602 DNTFFKSNINKMEDNTPKDILYESRNVSN-MNGNVLLGLNKNTHHDISTKDENHNDN 657	Qy 553 KKNLRDNI-KLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNK 601   :     :   :	878 FKVSLKEKKYIDNISNNMERVTYKNEMINEKISKMDDILYPCDKNKSLNMSCPVI	818 NYVKRKSNLYNNLSSNROSTVDMHNKYNSEEYINIQRTNKIYELSNKRIRNYKLYSMDEI	450

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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 C;Accession: T18444 R;Lawson, D.; Bowman, S.; Barrell, B.
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T18444
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A;Accession: T18444
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-1650 <LAW>
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Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Note: C0385c
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835 KDKNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIVIVNNNMGNNNSPRMKYGLCGSHTSID 894
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                                                                                                                                                                                       NIINKSFEKNN
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                                    QSEEYKKYGSNNKMDEMEIYNQHTN----DFNIN-----ENLNNKIYFDDYEGYDPEK 536
                                                                                                                                                NUNNINUNNI DVE------NYNNRDGTNNSMK-----
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                                                                         AYNSHNLFQPDNNKNTSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLN--NKEQ 834
                                                                                                               SSIKKKNNSSECLDEQKKKTYKYTIIEQKRYNFNDRDNNNAYIKDDTHKKEKGYYLNMIV 487
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Y, August 1997
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Pred. No. 3
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A;Title: Complex polymorphisms in an 330 kDa protein are A;Reference number: Z16556; MUID:98054002; PMID:9393853
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A; Cross-references: EMBL
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Best Local S
Matches 341
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дb		537 KKKLLDDHIYTQQKEYKNNINDILKDHHLNDKETKEKKNEIEIE 580
Ş	895 NMKNNEMKNNEMKDNEMKDNHI	KSNNNNSS 924
뫄	581 EEKKNKIEIEEEKKNKIEIEEEKKNKIE	EEKKNKIEIEEEKKNKIEIEEEKKOKIEIEEEKKKKIEIEEEKKKKIEMEEEKNKIDDEK 640
Qγ	925 SSSSSNNIYNNINDDD	TFQNDYCHNDNTF 954
Db	641 KNTYANDKIISHIDNVNCNIKIDALLDH	KNTYANDKIISHIDNVNCNIKIDALLDHIEEKKKTGHKEINLYKEIKNEYQKMLNDENSI 700
Ş	955 TIRKNNTN-INSNIYQNDDIIYTIN	TIRKKNNTN-INSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNED 1006
Db	701 MLEHEKKYNTHQVNNNLCDTKDMLQKEN	MLEHEKKYNTHQVNNNLCDTKDMLQKENKILTNNDKKKTFLLSKSKNITSNVLSSKIPGT 760
γQ	1007 IYNKEMEGKHIRLDDQDKY-DD	NDNNVDNNKNNVDNV 1045
Db	761 LSTKKLNATIKTIKKDVTDNEKKKYVHD	LSTKKLNATIKTIKKDVTDNEKKKYVHDHRKDNIIKRNKEFINIYKGKRNYANVEIGSEV 820
Ωу	1046 DNNVDNVDNVDKNVDN	DNNNVDNNV
망	821 CNNKVNVKGDDNKMMVENKQGDDNNMMV	CNNKVNVKGDDNKMMVENKQGDDNNMMVENKQGDENNVIVKNIERSESSFMFTHHRKNIT 880
Qy	1096DTIINNCLNSLDISSMYDDTKEIL	DTIINNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVIKKYINEDIKNMSLE 1149
Db	881 STSTDTCAKN-KEQIKYPHLYSNKNE	STSTDTCAKN-KEQIKYPHLYSNKNEDKDKKSIFLKNINENIKKNYKDKE 929
Qy	1150 EIDKTAQSIYEKRKVLLTKLLLLFKKNV	EIDKTAQSIYEKRKVLLTKLLLLFKKNVDTQINNETSDLRKDLVMCHICNNNPDDQF 1206
дb	930 KISTLEKKVFVKKDNVITNNDDEKHT	SSKINDDFNITIDKQKGKLNNNPVD 980
Qγ	1207 HFYAYSRLEKDIINLIMLRQ	HFYAYSRLEKDIINLIMLRQIWCESENLRLLYQFLVVEYQNKSANSVLLNVS 1258
Db	981LNRKIKNETKILEKDKSHMSKIQN	LNRKIKNETKILEKDKSHMSKIQNNLMKKKTNFPTNNKGISSTSISSS 1028
Qy	1259 SNNGDIILLNKKLVQDNIKNSMDHNNIH 1286	INNIH 1286
DЬ	1029 STKNFKDCGIIEKNKNLSNLKYTCIRNKMN 1058	NKMN 1058
PECIT.T 22		

probable chloroquine resistance protein CG2 (strain 7G8) - malaria parasite C;Species: Plasmodium falciparum C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000 C;Accession: T09079 (Plasmodium

linked

to Chloroquine-resistan

A;Status: translated from GB/EMBL/DDBJ

A; Experimental source: strain EMBL:AF030692; NID:g2642513; PIDN:AAC47853.1; PID:g2642514 ce: strain 7G8; from Brazil

----TFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILRV 184 IDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPG-KQNYLNFIKQKKKCAL----KKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDDTVDNFTVYENTIKPLI 79 Conservative 8.5%; 233; TSFNKKYAMKNEODMNKDDKNNELMIYLLIKIHSSGSLFFKIP 1307 Score 581; DB 2; Pred. No. 8.1e-17; 3; Mismatches 508 ----DLQYYINKRK-----NANYYEYPENYINNYI 1260 508; Length 2708; Indels 448; ----IFQYAAGDIF----128 77

880 PRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSSSSSSNN 931  2091 NMYTYSLINSTLTLNNIHLKRWKYLINTYCFNNYIMFFQTTQKYLLNRRLIKKAFFLRS 2150  932 NIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQNDDIIYTIN 979  :::   :::    :::    :::    :::	1874 EVFFFSPYFLPTVLYNLFEFLRTLGVWLTLLGRLKNDYTDINLRNDRNICNVFQYITAKK 1933  728 DAISCDNNMYPNITNNNNNNNNINNNNNNIDVENYN 764	NNNNNNNNNSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKN	303 SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKKSTCIN	1308 IKGKRYMKINNLDVIKNRELFIYH-KCLVINMKLEKKKKKYDNGKKNDDINTICM 1363  185 LTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAG 242
Db 1022 RŚ	Qy    DMTKYIERHEF I VDKVFDDTYDNFTYYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTY 103   DM	Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 Accession: T18402 Barale, J.C.; Candelle, D.; Attal-Bonnefoy, G.; Dehoux, P.; Bonnefoy, S.; fect. Immun. 65, 3003-3010, 1997 Title: Plasmodium falciparum AARP1, a giant protein containing repeated n Reference number: Z18929; MUID:97378065; PMID:9234746 Accession: T18402 Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-3844 eBBR> Cross-references: EMBL:Y08926; NID:e1154302; PID:e311435; PIDN:CAA70130.1 Genetics: Genetics: Genetics: Genetics: MBL:Y08926; NID:e1154302; PID:e311435; PIDN:CAA70130.1 Genetics: Aarp1 Query Match Best Local Similarity 20.7%; Pred. No. 1.2e-16; Best Local Similarity 20.7%; Pred. No. 1.2e-16; Best Local Similarity 20.7%; Pred. No. 1.2e-16; Genetics: Gaps		Db 2254 NGDDNKMNGDNKMNGDNKMNGDNKMNGDNKMNGDNKMNGDDNKINGDLANDDNKINGDLANDDNKINGDLANDDNKINGDNKINGDLANDNKINGDLANDNKINGDLANDLANDLANDLANDLANDLANDLANDLANDLANDLAN

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                                                                                                                                                                                                                                                                               KKKKKYMKGITICEYEKIKE---KNCICVLCKEGMSK-----NNLLAYICFSSHTNLLK
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                                       EREEKKKSKMIMMRGM--ESDNINEMVSDNINEMASDNINEM---VSDNINEMTSDNINE
                                                                          -RLEKDIINLIMLRQIWCESENLRLLYQFLVVEYQNKSANSVLLNVSSNNGDIILLN---
                                                                                                                    IANSFVVYIPKRYISENDKYRIYDCNEEEFFLDNSNKNLSELLKISKYSEERNYGIKRKK
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C;Species: Plasmodium falciparum
C;Species: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
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A; Residues: 1-2380 <GAR>
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  ---KNTSNIQNINTNKNN---QDGNVNYSMNFCHYNLND----
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ilarity 21.1%;
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Pred. No. 8.5e-17;
)8; Mismatches 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNDNGLMNKKKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414; Indels 510;
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                                                                              SHNLFQPDNN-----
    --KNYLIDLNNKEQKD
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: 1-25( ference ntal so : B0650w	Pertrea, M., Sali- ience 282, 1126-: Title: Chromosomu Reference number Accession: G7160! Status: prelimina Status: prelimina	al protein PFB0650w - malaria parasite (Plasmodium falciparum) Plasmodium falciparum -Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 N: G71609	Qy 1242VVEYQNKSANSVL-LNVSSNNGDIILLNKKLVQDNIKNSMDHNN 1284	Qy 1196 HICMNNPDDQFHFYAYSRLEKDIINLIMLRQIWCESENLRLLYQFL 1241     :	Qy 1136 KKYINEDIKNMSLEEIDKTAQSIYEKRKVLLTKLLLLFKKNVDTQINNETSDLRKDLVMC 1195   :   :   :         : :   :	Qy 1090YFQKNVDTIINNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVI 1135	Qy 1080 1089	Qy 1042 DNNVDNNNVDNNVDNNVDNNVDNNVDNDDDDVDFHNI 1079	Qy 994 EKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNNVDNNNKNNV 1041	Qy 962 TNIN 993 :  :  :   :	Qy 929 SNINNIYNNINDDDTFQNDYCHNDNTFTIRRKNN 961	Qy       903NNEMEDNEMEDNHIKSNNNNSSSSSS       928	Qy 882MKYGLCGSHTS	Qy 837 KNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIVIVNNNMGNNNSPR 881	Db 560 EKKNNKEVK-IMVDKNNDTEKDGNKKYDTSY-SFNIKNTLSKVFYKNYVKRKGMIKQQH 617
1201NPDDQFHFYAYSRLEKDIINLIMLRQIWCESENLRLLYQFLVVEYQNKSAN	QY 1099 INNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVIKKYINEDIKNMSL 1148	Qy 985 MSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNNVDNNNK-NNV 1041	Qy 926 SSSSNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTYNINSNIYQNDDII-YTINSLNDY 984 ::    :	Qy 869 IVNNNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSSS 925	OY 812 SMNFCHYNLNDKNYLIDLNNKEQKDKNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIV 868	Qy 768GTNNSMKLYAAVNSHNLFQPDNNKNTSNTQNINTNKNNQDGNVNY- 811	Oy 720 KUNDNIFFDAISCDNNMYPNITNNNNNNNNNNNNNNNNNID767	Qy 667 INNSNVNSINNS-NMNSINNSNMNSNSIYKSNYNSNQSISDVQIRYV-NEMDTSN 719	Qy 615 DNTPKDILYESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKINNGVINI 666	Qy 571 IMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKME 614 ::	Qy 513NSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSSCDN 570	Qy 464 NNDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Qy 411 EGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYNDNTINKKHNNNNNNNND 463 ;     ;   ; ; ; ;   ;   ;	Qy 355 LDSKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPR 410	Best Local Similarity 24.1%; Pred. No. le-16; Matches 248; Conservative 164; Mismatches 389; Indels 229; Gaps 52;

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A; Molecule type: DNA
A; Residues: 1-2010 <AR>
A; Cross-references: GB: AE001391;
A; Experimental source: clone 3D7
C; Genetics:
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 KDINKNTSLGKIAFIDLAGSERGADTVSQNKQTQ---TDGANINRSLLALKECIRAMDSD
                                    APVKNYIIGENLCGENGCGKNGCGDILRGDILCGDILRGDNNSIPLFRSNRIFCKQS---
                                                                                                                                                                                                       NYAFTOTSDFSSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSNYSCCYLNNECFVKNISICKKCMFSYFEFKNVTKVIYMRHGARTPKKKIKNIWPFKEG
                                                                                                                                                                                 SFNYADMLKYTKYYYKNILKDKKNIYTNNKKKELFFPLMEHLYMYKKKLLIN-KMKEK--
                                                                                                                                                                                                                                                       NNNNDSSSMVNNMINHMINNNINNNINNNNNNNNNNNNH-------LPQP
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                                                                                                                                                                                                                                                                                                                                                                            KKCKTLYKNKYNNNNNNNNNNYVINEKYNGSNKNDYVKNNTYD--NKGYSYLYDLSTSFN
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                                                                                 --ILFFKSNYDKTNDNNIDTYTKRKEKKKCLNKRSKCFQNWILNRDITSGQYNCID-KNT
                                                                                                        KUNTFFKSNINKMEDNTPKDILYESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKIN
                                                                                                                                --NIKKKKKYDKIIKLINKYLCIKTINSERCKLTAYGIICGILGISEYIYFFFF----
                                                                                                                                                         CDNIMNKKKON---
                                                                                                                                                                                                                                                                              INKMKKIKNKNMNNYNKCYIKFSSIRKRGYHKMENIECNNKNNDDDNNDDNNNNNNNDDNN
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                                                                                                                                                       -NLHLARHSVGS---KLT----
                                                                                                                                                                                                                               -NNDONNNUNNNDDNNNNNDDDNNYYYYNYNNDETPFNNK
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Pred. No. 1.8e-16;
2; Mismatches 404
                                                                                                                                                                                                      -DDMNCHLNNNDKSIF-----LHKKNLRDNIKLKNRSS
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                                                        -SINNSNMISNSIYKSN-YNSNQSISD
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R;Su, X.Z; Kirkman, L.A.; Fujioka, H.; Wel
Cell 91, 593-603, 1997
A;Title: Complex polymorphisms in an 330 kl
A;Reference number: Z16556; MUID:98054002;
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                                                                                                                                                                                                                                          probable chloroquine resistance protein C;Species: Plasmodium falciparum C;Date: 13-Aug-1999 #sequence_revision 1 C;Accession: T09080
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                                                                                  C; Keywords:
                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-2819 <SUX>
                                                                                                                                                                              A; Accession: T09080
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                                                                                                                      A; Experimental source:
                                                                                                                                A; Cross-references:
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                                Best Local
Matches 34
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                                              Query Match
Best Local
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al Similarity 19.8%;
345; Conservation
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KKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDDTVDNFTVYENTIKPLI
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                                                                                  resistance
                                                                                                                      EMBL:AF030693;
ce: strain HB3;
                                                                                                                                                                     GB/EMBL/DDBJ
                                    244;
                                   Score 567; DB 2;
Pred. No. 3.2e-16;
4; Mismatches 490
                                                                                                                                                                                             330 kDa protein are
54002; PMID:9393853
                                                                                                                                                                                                                                                        13-Aug-1999
                                                                                                                                                                                                                                Wellems,
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                                     490;
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LNDKNYLIDLNNKEQKDKNIHG--CDNN--IIQNRNDFEKKKK-----TNFYNNNNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNKIYQDKIKNWTYHPFHNKKKNVKIIKKF-ISAYDAYIYHGVNLNLNFNRAYEKLSQHP
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                                                                                                                                                                                                                       NID:g2642515; PIDN:AAC47854.1; PID:g2642516 from Honduras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG2 (strain HB3) - malaria parasite (Plasmodium
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601 KDNTFFKSNINKMEDNTPKDILYESRNVSNMNGNV	80 IDLYENGCYCSCFAYGOTGSGKTYTMLGSGPYGOSDTPGNANYYEYDENYINNYI 1267  80 IDLYENGCYCSCFAYGOTGSGKTYTMLGSGPYGOSDTPG
RESULT 28 B71612 hypothetical protein PFB0555c - malaria parasite (Plasmodium falciparum) C.Species: Plasmodium falciparum C.Species: Plasmodium falciparum C.Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C.Accession: B71612 R.Gardner, M.J., Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelinin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelinin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelinin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelinin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelinin, E.V; Pertea, M.J.; Tettelinin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V; Pertea, M.J.; Tettelinin, E.V; Pertea, M.J.; Tettelinin, E.V; Pertea, M.J.; Pred. No. 6.5e-16; Matches 352; Conservative 246; Mismatches 541; Indels 573; Gaps 82; Ouery Match .;	07   07   07   07   07   07   07   07

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	839 IHGCD-NNIIQNRNDFEKKKKTNFYNNNNIVIVNNNM
	793 SNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLNNKEQKDKN 838 
·	746 NNINININININININITOVENYNINFOGTINISKKLYAYNSHILFQPDINIKNT 792
	694 YKSNYNSNQSISDVQIRYVNEMDTSNKNNDNIFFDAISCDNNMYPNITNNNN 745
י תי עי עי ע	660 NNNSNMNSNSI 693
יו בי פי פי פ	613MEDNTPKDILYESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKI 659
#1 O O O O	585SVGSKLTMFSYDDQKNKDNTFFKSNINK 612
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	511 NNNSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKL 562 
	484 NNMINHMINNNINNNINVNNNNNNNNNN 510 
	433 KKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
	375NHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPREGFTSTFGKYSSLNDIDKIKKN 432 
, ט	327 YSSRVKNIFKNKSTCINEEDDTNTERISILDSKGSEMNASSIENVVIKS 374
	267 LLALKECTRAMDSDKNHIPFRDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLR 326
o U 1	208 QNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGSERGÅDTVSQNKQTQTDG-ANINRS 266
	167 LENGKKEVVVK
) U K	116 TPGIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAA 166  : :    : :
	59KVFDDTVDNFTVYENTIKPLIIDLY-ENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSD 115
	778 VEKLAQEEGNITKKNHKNIHMVILEDTLYYKIIYILRKKNINKDTIYITYIEYYYILLDY 837

	SSYNNNYNIYNNTNNFYEYHDYIAIKNILHKK 2356	Db 2325
	IILLNKKLVQDNIKNSMDHNNIHKK 1288	Qy 1264
2324	ISYIDDDHLINNMLHLLRRKNIYYKYVLNINEYNNFLDNHKCKRKRKFINYNNIQ	Db 2270
1263	-SRLEKD-IINLIMLRQIWCESENLRLLYQFLVVEYQNKSANSVLLNVSSNNGD	Qy 1212
2269		Db 2214
1211	1170 LLLFKKNVDTQINNETSDLRKDLVMCHICNNNPDDQFHFYAY 1211	Qy 117
2213		Db 2154
1169	KAEKDNVIKKYINEDIKNMSLEEIDKTAQSIY-EKRKVLLTKL 1169	Qy 1128
2153	DEQRESELWNIVECLEYNVINKLHVNSINCLKKNKLGSY	<b>D</b> ხ 2115
1127		Qу 1068
2114		Db ·2058
1067	DDQDKYDDNNINYDNNINKANIVDNNIVDNNIVDNNIVDNNIVDNNIVDNNIV 1067	Qy 1020
2057		Db 2001
610	IYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRL 1019	Qy 968
2000	KYSSGYLPLERIIKLFMDVIFGHFIKFININENINDYELLEVLEYNGNKCYELLRFLFFF	Db 1941
967	TINSN	Qу 962
940		Db 1881
)61	NIYNNINDDDTFQNDYCHNDNT-FTIRRKNN 961	Qу 932
.880	NGNQNVINIKDEDKHITNIKDGDKHITNIKDGDKNITNIKDDDKNITNMKKKNNKN 1880	Db 1825
931		Qy 875

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RESULT 29
A42640
A42640
Kinesin-related protein KIP1 - yeast (Saccharomyces cerevisiae)
Kinesin-related protein YBL0504; protein YBL0521; protein YBL063w
N;Alternate names: protein YBL0504; protein YBL0521; protein YBL063w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: A42640; 39826; S45798; S37327
C;Accession: A42640; S45798; S37327
R;Roof, D.M.; Meluh, P.B.; Rose, M.D.
J. Cell Biol. 118, 95-108, 1992
A;Title: Kinesin-related proteins required for assembly of the mitotic spindle.
A;Reference number: A42640; MUID:92317166; PMID:1618910
A;Accession: A42640

A;Molecule type: DNA
A;Residues: I-1111 <ROO>
A;Residues: I-1111 <ROO>
A;Residues: I-1110
A;Cross-references: EMBL:Z11962; NID:g3850; PIDN:CAA78019.1; PID:g3851
A;Note: sequence extracted from NCBI backbone (NCBIN:107715, NCBIP:107718)
A;Note: sequence extracted from NCBI backbone, F.; Dubois, E.; Messenguy, F.
Yeast 9, 1355-1371, 193
A;Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of y.
A;Reference number: S39824; MUID:94205266; PMID:8154187

A;Accession: S39826

A; Molecule type: DNA A; Residues: 1-1111 <SCH>

A;Cross-references: EMBL:Z23261; NID:g313733; PIDN:CAA80785.1; PID:g313736
R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, submitted to the Protein Sequence Database, August 1994
A;Reference number: S45782
A;Accession: S45798

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A;Molecule type: DNA A;Residues: 1-1111 <DUB> A;Cross-references: EMBL:Z35824; NID:g536098; PIDN:CAA84883.1; PID:g536099; GSPDB:GN000

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C;Genetics:
A;Genetics:
A;Genes: SGD:KIP1; MIPS:YBL063w
A;Genes: SGD:S0000159; MIPS:YBL063w
A;Cross-references: SGD:S0000159; MIPS:YBL063w
A;Map position: 2L
C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; F;53-416/Domain: kinesin motor domain homology <KMOT>
F;141-148/Region: nucleotide-binding motif A (P-loop)
F;147/Binding site: ATP (Lys) #status predicted
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   VLTSIKKFQNIICSDIALTNEKIMSLIDEIQ----
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                                   NMNSINN-SNMNSNSIYKSNYNSNQSISDVQIRYVNEMDT-SNKNNDNIFFDAISCDNNM
                                                                           KTVSQNNESFTNDLISLSRGMNMDISSKLRSLPINEFLNKISQTICETCGDDNTIA-SNP
                                                                                                                                                    RSEFHDELNKCIDNLKDKOSKLDODIWOKTASIFNETDIVVNKIHSDSIASLAHNAENTL
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Pred. No. 2e-1:
04; Mismatches
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R;Li, W.B.; Bzik, D.J.; Tanaka, M.; Gu, H.M.; Fox, B.A.; II
MOl. Biochem. Parasitol. 46, 229-239, 1991
A;Title: Characterization of the gene encoding the largest A;Reference number: A45597; MUID:92018020; PMID:1656254
A;Accession: A45597
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A;Rote: sequence extracted from NCBI backbone (NCBIN: C;Superfamily: Plasmodium DNA-directed RNA polymerase
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                                                                              NSVLLNVSSN--NGDIILLNKKLVQDNIKNSMDHNNIHKK 1288
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hypothetical protein - malaria parasite (Plasmodium falciparum)

(;Species: Plasmodium falciparum

(;Ante: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000

(;Anccession: T28150; S23688

R;Kun, J.F.; Hibbs, A.R.; Saul, A.; McColl, D.J.; Coppel, R.L.; Anders, R.F.

Mol. Biochem. Parasitol. 85, 41-51, 1997

A;Title: A putative Plasmodium falciparum exported serine/threonine protein kinase.

A;Reference number: Z20482; MUID:97262159; PMID:9108547

A;Accession: T28150
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A;Molecule type: DNA
A;Residues: 1-2510 <KUN>
A;Crossives: 1-2510 <KUN>
A;Crossives: EMBL:U40232; NID:g1658332; PID:g1658333; PIDN:AAB54058.
A;Crossives: EMBL:U40232; NID:g1658332; PID:g1658333; PIDN:AAB54058.
A;Experimental source: strain FCQ27/PNG
R;Kun, J.; Hesselbach, J.; Schreiber, M.; Scherf, A.; Gysin, J.; Mattei, D.
Res. Immunol. 142, 199-210, 1991
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A;Residues: 241,'S',243-244,673-959,'R',961-977,'S',1493-1494 <KU2>
A;Cross-references: EMBL:X53019
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C;Keywords: surface antigen
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Matches 355;
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                          QPNYAFTDTSDFSSLDDMN-----
                                                                                   ISNNMSSNLFLKSLISNNFIPDHLIPNNSNSKNIISNNVNLNNFVSNNFTSNHMEYNNRK
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KLLQNLLYHRKKEYEKKKKVNKILKLIHICFGRKYHCFESLFNLECIGLCYKKL--KNMK
                              LLYQFLVV----EYQNKSANSVLLNV------
                                                                   NEFKFLREQELLCHFNCN
                                                                                                  NETSDLRKDLVMCHI-CNNNPDDQFHFYAYSRLE----
                                                                                                                                      EKNKDNEKSINKNTNKLNEKELVILESDLMLNNKLDNCLCCHKKRYFELAVKEIDISRKG
                                                                                                                                                                    IKNMSLEE-IDKTAQSIYEKRKVLLTKLLLL----
                                                                                                                                                                                                      CHMKKGLKYLVDKYDIASDSDCVSYWNDYYLELKDHLDDEKYEEITKETKNVQKV---QD
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A;Gene: C0440c
A;Map position:
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Matches 273; Conserv
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73 NTIKPLIIDLYENGCVCSCFAYGOTGSGKTYTMLGSQPYGQSDTPGIFQYAA	Query Match 7.9%; Score 543; DB 2; Length 1984; Best Local Similarity 21.5%; Pred. No. 2.2e-15; Matches 321; Conservative 202; Mismatches 412; Indels 560; Gaps 73;  Qy 2 KOSDIITVKNNCTLYIDEPRYKUDMTKYIERHEFIVDKVFDDTVDNFTVYE 72	A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-1984 <kri> A;Note: sequence extracted from NCBI backbone (NCBIP:122678)</kri>	-398, 1993 ation ATPase-like molecules from Plasmodium falciparum. 4396; MUID:93132070; PMID:8421054	parum  Pe_revision 18-Nov-1994 #text_change 09  Pe_revision 18-Nov-1994 #text_change 09	RESULT 34 P-type Cation translocating ATPase - malaria parasite (Plasmodium falciparum)	Db 1082 CKNEISHSHAENK 1094	1030 EIYTHSLHLLYLYIL	Qy 1226 QIWCESENLRLLYQFLVVEYQNKSANSVLLNVSSNNGDIILLNKKLVQDN 1275	Qy 1172 LFKKNVDTQINNETSDLRKDLVMCH-ICNNNPDDQFHFYAYSRLEKDIINLIMLR 1225	939 KHNDTDINIFLSSNIÄESSITIPNVRLVIDFCIQKNIEVNDKKKAHILVKK	1120 NNILLSKYKAEKDNVIKKYINEDIKNMSLEEIDKTAQSIYEKRKVLLTKLLL 11	Qy 1064 N-NNVDNDDDDDVDFHNIKNFNNNEYLSYFQKUVDTIINNCLNSLDISSMYDDTKEIL 1119	Qy 1013 EGKHIRLDDQDKYDDNDNNNVDNNNKNNVDNNVDNNVDNNVDNNVDNNVDNNVDNNV	CY 973 D-IIYILNSLUYMSNITLLHEKEKYTYPTLSTNEDIINKEM 1012    : :           :       :       :   :     : :   :	724 EKINDEKINDDNKKSCDDKKSCDGNNNFVKESVIDFILRKNCNKINLSKNS	Qy 932 NIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQND 972	Db 664 FYSYFEHPNIKMGSIFIGTKIFSIDTFYIEDIINYTRYGSRNIHDEKINDEKINDEKIND 723	Qy 912 912 912 912 912 912 913 914 915 915 915 915 915 915 915 915 915 915	Qy 889	544 INIIVTEPRRI
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Qy       645 HDISTKDENHNDNKINNGVINIINNSNMMSINNSNMSIYKSNYNSNQ 702         1	Qy       496NNNINVNNNNNNNNNNNNNNNNNNNNNNNNNNNN	341 INEEDDTNTERISILDSKGSEMNASSIENVVI	T18502 T18502 T18502 T18502 Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000 C;Accession: T18502 R;Lawson, D:; Bowman; S:; Barrell, B. submitted to the EMBL Data Library, August 1997 A;Reference number: Z18935 A;Accession: T18502 A;Accession: T18502 A;Kstatus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Cross-references: EMBL:Z98551; NID:e1331903; PID:e1331923; PIDN:CAB11141.1 C;Genetics: A;Mosp position: 3 A;Note: C0755c Query Match 7.9%; Score 542.5; DB 2; Length 1553;	QY 1060 NNVDNNNVDNDDDVDFHNIKNFNNNEYLSYFQKNVDTIINNCLNSLDISSMYDDTKEIL 1119
236; 3 SKI 59 TNI 56 IVI	A;Gene: cut7 A;Introns: 50/1 C;Function: A;Description: probably involved in mitotic spindle body duplication A;Description: probably involved in mitotic spindle body duplication C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology C;Keywords: ATP, microtubule binding; mitosis; nucleotide binding; P-loop C;Keywords: ATP, microtubule binding; motosis; nucleotide binding; P-loop F;61-415/Domain: kinesin motor domain homology <kmot> F;147-154/Region: nucleotide-binding motif A (P-loop) F;153/Binding site: ATP (Lys) #status predicted Query Match Query Match Output Match O</kmot>	Kinesin-related protein cut? - fission yeast (SChizosaccharomyces pomber) C;Species: Schizosaccharomyces pombe C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Feb-2001 C;Accession: \$14032 R;Hagdan, I.; Yanagida, M. Nature 347, 563-566, 1990 A;Title: Novel potential mitotic motor protein encoded by the fission yeast cut7(+) gen A;Reference number: \$14032; MUID:91015362; PMID:2145514 A;Accession: \$14032 A;Molecule type: DNA A;Residues: 1-1073 cHAG> A;Residues: 1-1073 cHAG> A;Note: the authors translated the codon GCC for residue 2 as Gly and AGT for residue 1: C:Generics:	Qy 1014	Qy 752NNNNNIDDE-NYNNRDGTNNSMKLYAYNSHNLFQPDNNKNTSNIQNINTNKN 803

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 SKRELPATPSWTRDSSLIKETTNLN--LDSDKKFVRETYTSSNOSNEPDVYDK 1051
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                                                          HTELQKITDHVLKGTTSLANHTNELLGLGDESLCNLETTIEDTSLVK-----LETTGDTP
                                                                                                                   EVQTLDRLLQKVKEHSEDNTKEKHQQLLDLLESLVGNNDN---
                                                                                                                                                                           ASQAEIVGANKERIOKTVENGSQL----LDSKSKAIHSNSRSMYDHCLALAESOKOGVNL
                                                                                                                                                                                                                                                                                                TTSLNDADIILSDYISDQKSKFESKQQDLIANIGKIVSNFLQE-----QNESLYTKA--
                                                                                                                                                                                                                                                                                                                        MNSINNSNM---NSNSIYKSNYNSNQ-----SISDVQIRYVNEMDTSNXNNDNIFFDAIS 731
                                                                                                                                                                                                                                                                                                                                                       QLVQELRSLYNL-----QHTHEE-----SQKELMYGVRN-----DIDALVKTC
                                                                                                                                                                                                                                                                                                                                                                                                                   ----SKNSLLDALEHSLQDISMSSQKLGNGISSELIELQKDMKESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKEYIASLYEKLDRTERNNKENENNFWNLKFNLLTMLRSFHGSFTDETNGYFTLLNDFNA
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                           RKNNTNINSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNK 1010
                                                                                      EMKNNEMKDNEMKDNHIKSNNNNS--SSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIR
                                                                                                                                             IIQNRNDFEKKKKTNFYNNNN-----IVIVNNNMGNNNSPRMKYGLCGSHTSIDNMKNN 899
                                                                                                                                                                                                        TSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLNNKEQKDKNIHGCD-----NN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVYLAESTYKELMDRVQNKDLLCQEQARKLEVLDLNVKSSREQLQYVSKSNQEHKKEVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSHSIFTITLHRKVSSGMTDETNSLTINNNSDDLLRASKLHMVDLAGSENIGRSGAENKR
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                                                                                                                                                                                                                                       ----DILHSHLNDTNSNIRKANEI-----MNNRSEEFLRNA-------
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RESULT

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732

QLVQELRSLYNL--

-QHTHEE-----SQKELMYGVRN-----DIDALVKTC

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kinesin-like protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec1999 #sequence_revision 03-Dec-1999 #text_cC;Accession: T38378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDE A;Molecule type: DNA A;Residues: 1-1085 <MCL>A;Cross-references: EMBL:Z70691; PIDN:CAA94636.1; A;Experimental source: clone c25G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T38378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Genetics:
;Gene: SPDB:SPAC25G10.07c
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                                                                                                                                                                                                                                                          SKEYIASLYEKLDRTERNNKENENNFWNLKFNLLTMLRSFHGSFTDETNGYFTLLNDFNA
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  DILYESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKINNGVINIINNSNVNSINNSN
                                                                                                                                                        SMEELLNTHSNQL---LISMTKITEHFQSLDEALQSARSSCAVPNS--SLDLIVSELKD-
                                                                                                                                                                                                        NNNNNNNSHNNHLPQPNYAFTD-TSDFSSLDD-----MNCHLNNNDKSIFLHKKNLRDN
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                                                                                                      **IKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKMEDNTPK
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                                                         -SKNSLLDALEHSLQDISMSSQKLGNGISSELIELQKDMKESY
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Pred. No. 1.8e-15;
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Qy 486MINHMINN-NINNNINVANNINNINNINNINNINHLPOPNYAFTDTSDFSSLDDMN 539	Qy       367 IENVVIKSNHL	243 SERGADTVSQNKQTQTDGANINR-SILALKECIRAMDSDKNHIPFRDSELTKV   :	Query Match Query Match Page 15, Best Local Similarity 21.6%; Pred. No. 3.6e-15; Best Local Similarity 21.6%; Pred. No. 3.6e-15; Matches 326; Conservative 225; Mismatches 488; Indels 469; Gaps 77;  Qy 137 DNTKGIFISFYEI-YCGKLYDLLQ	RESULT 39 E71619 C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000 C;Accession: E71619 R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; R; Pertea, M.; Salzberg, S.; Zhou; L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998 A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551 A;Accession: E71619 A;Accession: E71619 A;Restdus: preliminary; nucleic acid sequence not shown; translation not shown A;Residus: 1-1516 cGAR> A;Residus: 1-1516 cGAR> A;Cross-references: GB:AE001383; GB:AE001362; NID:g3845135; PIDN:AAC71842.1; PID:g384513 A;Experimental source: clone 3D7 C;Genetics: A;Gene: PFB0265c
RESULT 40  RESULT 40  T47525  Kinesin-related protein-like - Arabidopsis thaliana N,Alternate names: protein F16L2.60 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C;Accession: T47525 R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, March 2000 A;Reference number: Z24468 A;Accession: T47525 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1058 <jor> A;Cross-references: EMBL:AL162459 A;Experimental source: cultivar Columbia; BAC clone F16L2</jor>	1182 NNETSDLRKDLYMCHICKNN-PI-DOFHFYAYSRLEKDIINLIMLRQIWCESENLR 1235	1047 NNNVDNNVDNNVDNNVDNNVD-NDDDDVDFHNIKNFNNNEYL	Qy 912 KDMHI	693 IYKSNY-NSNQSISDV-QIRYVNEMDTSNKNNDNIFPDAISCDNNMYPNIT

KYQDLYVKGEESKEDIKNQIDFVTQECYRNNDIIRDTHDKSDIFKNIKIDNNKKYEIY	778
IDVENYNNRDGTNNSMKLYAYN	779
FFLKIENEFKKDLLLDDSQIFGDSLLADIKEYNYT	838
TNKNNQDGNVNYSMNFCHYNLNDKNYLIDL	830
NEPITNEYEEKNNIIYISDEQKYNEEDIIFKD	893
NNIIQNRNDFEKKKK	858
YVNEKIEEYNNKNDDKSSSSSIILEEIKYKKEKK	953
SPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEM	911
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1003
NSSSSSSNNNIYNNINDDTFQNDYC	948
LEESKFODNUNIYONDDELEKNUSKDYISDVDK	1061
YQNDDIIYTINSLNDYMSNTLLHFKEKY	996
QSTESHKSNEFICTENKSLRKQYMSKEDI	1115
QDKYDDNDNNVDNNVD	1046
KKQVMDNFQMNIEQNNDKLKEDKLDEGAYFEYLED	1175
DNNNVD-NDDDDVDFHNI KNFNNNEYL	1088
KKNNIEINDEMNDDIKLLLNFFGIPYIQSPCEAEA	1235
SMYDDTKEILNNILLSKYKAEKDNVIKKYI	1139
GKTVIKNFFNKKKTVEVYEKKAIEEKLGLY	1290
EEIDKTAQSIYEKRKVLLTKLLLLFKKNVDTQI	1181
NALEIIKAFPN-FEDLKILKDIVSNPFRK-IDKNM	1348
PD-DQFHFYAYSRLEKDIINLIMLRQIWCESENLR	1235
KKFEWHVP	1402
NSVLLNVSSNNGDIILLNKKLVQDNIKNSM	1280
QKYNVNVRTYQSKIEDFFPLLEKKRKTVDDLIDHI	1462

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A;Map position: 3
A;Matposition: 3
A;Introns: 56/2; 99/3; 151/3; 310/3; 343/2; 395/3; 419/1; 444/3; 462/3; 489/3; 527/1; A;Note: F1612.60
C;Superfamily: kinesin-related protein KIP1; kinesin motor domain homology
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  I QNRNDFEKKKKTNFYNNNNI VI VNNNMGNNNS PRMKYGLCGSHTS I DNMKNNEMKNNEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IERLE-LQSESKDKRVVDLQELYNSQQILTAELSEKLEKTEKK-LEETEHSLFD---LEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALENGKKEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKD 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLL------QKRKWVA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFGPASQQKDLYDQAICPIVFEVLE-GYNCTIFAYGQTGTGKTYTMEGGARKKNGEFPSD 158
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                                                                                                                                                                                                   LOSSLNKQEEKLITFAQQQRKAHSRAVDTARSVSKVTVEFFKTLDTHATKLTGIVEEAQT
                                                                                                                                                                                                                                       NMNSINNSN-----MNSNSIYKSNYNSNQSISDVQIRYVNEMDTSNKNNDNIFFDAIS 731
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SSDVSNLFSKIERKDKIEDGNRFLIQKFQ 573
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                                           TTLQHEMSTMQDSTSSIKAEWSI----HMEKTESSHHEDTSAVESGKKAMQEVLLNCLEKT
                                                                                TSNIQNINTNKNNQDG-NVNYSMNFCHYNLNDKNYLIDLNNKEQKDKNIH----GCDNNI
                                                                                                                                                            CDNNMY PNI TNINNNNNNNNNNNNNNN I DVENY NNR DGTNNSMKLY AYNSHNL FOPDNIKN
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Search completed: October 2, 2003, 16:21:28
Job time : 94 secs

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         Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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TITLE OF INVENTION: KINI-3 MOTOR PROTEIN AND ME
FILE REFERENCE: 020552-002400US
CURRENT APPLICATION NUMBER: US/09/967,908A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/675,227
PRIOR TILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Applic Patent No. 6514738
                                                                             Sequence 2, Application US/09967908A Patent No. 6514738 GENERAL INFORMATION:
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Best Local
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       APPLICANT:
                                     APPLICANT: Cytokinetics, Inc. APPLICANT: Beraud, Christoph
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ORGANISM: Artificial Sequence
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Freedman, Richard
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Guo, Jun
Freedman, Richard
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Pred. No. 6.8e-49;
8; Mismatches 116
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; APPLICANT: Davies, Katherine A.
; TITLE OF INVENTION: KINI-3 MOTOR PROTEIN AND ME
; FILE REFERENCE: 020552-002400US
; CURRENT APPLICATION NUMBER: US/09/967,908A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 09/675,227
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 10
                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 343
TYPE: PRT
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APPLICANT: Beraud, Christopher
APPLICANT: Guo, Jun
APPLICANT: Freedman, Richard
APPLICANT: Patel, Umesh A.
APPLICANT: Davies, Katherine A.
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: KINI-3 MOTOR PROTEIN AND METHODS
FILE REFERENCE: 020552-002400US
CURRENT APPLICATION NUMBER: US/09/967,908A
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/675,227 PRIOR FILING DATE: 2000-09-29
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                                                                                                                                          NUMBER OF SEQ ID NOS: 10
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                         ORGANISM: Artificial Sequence FEATURE:
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       OTHER INFORMATION: Description of Artificial Sequence: Peptide
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APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: KINI-3 MOTOR PROTEIN AND METHODS FOR
FILE REFERENCE: 020552-002400US
CURRENT APPLICATION NUMBER: US/09/967,908A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/675,227
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NOME: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 373
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US-09-967-908A-4
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                                                                                                                                                  US-09-967-908A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application Patent No. 6514738 GENERAL INFORMATION:
                                                                                                              Query Match
Best Local :
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                                                                                                                                                          FEATURE: FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fragment OTHER INFORMATION: encoding residues D183-L546 with flanking vecother INFORMATION: sequence.
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                            Local
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                                             4 KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
                                                                                                          Similarity
                TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA
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                                                                                               Conservative
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                                                                                              Score 758.5; DB 4
Pred. No. 3.6e-48;
8; Mismatches 103
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Pred. No. 3.2e-48;
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                                                                                                                       DB 4;
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                                                                                                                     Length 373;
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US-09-291-170A-3
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LENGTH: 730
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APPLICANT:
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    Application US/09291170A
    6410687

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42.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Xenopus laevis
FEATURE:
OTHER INFORMATION: Xenopus kinesin central motor 1
   809
                                                                                                                                                                                                                                                                                                                                                                                                   179 LKILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSL-GKIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 RICVCVRKRPLNKQELSKKEIDIISVPSKNIVLVHEPKLKVDLTKYLENQAFRFDFSFDE
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                                                                                                                     DSFIGENSRTCMIAMLSPGFNSCEYTLNTLRYADRVKELSPQNA-----ETNDDNLQME
DSGGSH----ASIEGLQLQDDFLLKDEELSTHN--SFQDALNRVGELEDKAVDELRE
                                                         DSKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPRE
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The Regents of the University of California
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Pred. No. 9:3e-48;
4; Mismatches 130
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APPLICANT: Hartman, James J.

APPLICANT: The Regents of the University of California

FITLE OF INVENTION: Assays for the Detection of Microtubule

FITLE OF INVENTION: Depolymerization Inhibitors

FILE REFERENCE: 185578-000510US

CURRENT APPLICATION NUMBER: US/09/724,884

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/291,170

PRIOR APPLICATION NUMBER: 09/291,170

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS

LEVENTIA DATE: 1991-04-13
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; Sequence 12, Application US/09594669
; Patent No. 6331424
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US-09-724-884-3
                                                                                                                                                                                                                                                                              RESULT 8
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Best Local :
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APPLICANT: Hartman, Jan
                                                                              APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6331424el motor
TITLE OF INVENTION: their use
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/295,612
                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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ORGANISM: Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 11.1%;
Similarity 42.1%;
75; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVDLAGNERGVDTASADRITRMKGAEINRSLLALKECIRALGQNKSHTPFRESKLTQILR
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                                                                                                                                                                                                                                                                                                                                                                                            DSKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPRE 411
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                                                                                                                                                                                                                                                                                                                                              DSGGSH---ASTEGLQLQDDFLLKDEELSTHN--SFQDALNRVGELEDKAVDELRE
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                                                                                                                proteins
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4 KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD

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; SEQ ID NO 10
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Human
US-09-594-669-10
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US-09-594-669-12
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US-09-594-669-10
Query Match
Best Local Similarity
Matches 174; Conserv
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APPLICANT: Beraud, Christophe
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                              APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6331424el motor proteins
TITLE OF INVENTION: their use
FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/295,612
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PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 16
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-0
PRIOR APPLICATION NUMBER:
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TYPE: PRT
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Local Similarity 42.1%; Pred. No. 1.1e-47;
hes 174; Conservative 75; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 EHLVNSADD-VIKMIDMGSACRTSGQTFANSNSSRSHACFQIILR--AKGRMHGKFSLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AAGDIFTFLN--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK 180
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5. 6331424
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                                                                                                                                                                        FastSEQ for Windows Version 4.0
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           Conservative
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           75;
       Score 752.5; DB 4
Pred. No. 1.2e-47;
75; Mismatches 143
                                           DB 4;
           143;
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FILE REFERENCE: 1042
FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/295,612
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: US 09/314,464
PRIOR FILING DATE: 1999-05-18
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US-09-594-669-8
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                                                                                                                                                                                                                                                                                                                      Matches 174;
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 8
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APPLICANT: Beraud,
APPLICANT: Sakowic:
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6331424el motor proteins and methods
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 473
   240
                                    249
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                                                                                                                               AAGDIFTFLN--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK 180
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 LAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIF 299
                                                                   ILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFID
                                                                                                                                                                                                     TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGFFQY 122
                                                                                                                                                                                                                                               RICVCVRKRPLNKQELAKKEIDVISIPSKCLLLVHEPKLKVDLTKYLENQAFCFDFAFDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEEMEACS--NGALIPGNLSKEEEELSSQMSSFNEAMTQIRELEEKAMEELKE
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                                                                                                      ASRDVFILKNQPCYRKLGLE-VYVTFFBIYNGKLFDLLNKKAKLRVLEDGKQQVQVVGLQ
                                                                                                                                                                           TASNEVVYRFTARPLVQTIFEGG-KATCFAYGQTGSGKTHTMGGDLSGKAQNASKGIYAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGENSRTCMIATISPGISSCEYTLNTLRYADRVKELSPHSGPSGEQ-----LIQME
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42.1%; Pred. No. 1.4e-47;
ative 75; Mismatches 143;
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RESULT 12
US-09-594-669-16
; Sequence 16, Application US/09594669
; Patent No. 6331424
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US-09-594-669-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: No. 6331424el motor proteins and methods for TITLE OF INVENTION: their use FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/295,612
PRIOR PILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 16
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TYPE: PRT
ORGANISM: Human
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                                                                                                              300 VGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSK 358
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                                       GSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPRE 411
                                                                                                                                                                 LAGNERGADTSSADROTRMEGAEINKSLLALKECIRALGONKAHTPFRESKLTOVLRDSF
                                                                                                                                                                                                                                                                                                                                                                               AAGDIFTFLW--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK 180
                                                                                  IGENSRTCMIATISPGISSCEYTLNTLRYADRVKELSPHSGPSGEQ.
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-NGALIPGNLSKEEEELSSQMSSFNEAMTQIRELEEKAMEELKE
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42.1%; Pred. No. 2.6e-47;
tive 75; Mismatches 143;
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CURRENT APPLICATION NUMBER: US/09/594,669
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/295,612
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: US 09/314,464
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 725
; TYPE: PRT
; ORGANISM: Human
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US-09-595-684B-33
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APPLICANT: Wood, Kenneth
APPLICANT: Yu, Ming
TITLE OF INVENTION: Human kinesins and method
TITLE OF INVENTION: and purifying human kine
FILE REFERENCE: cytop036
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Beraud, Christophe
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Best Local :
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APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6331424el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1042
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APPLICANT:
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Local Similarity 41.9%;
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VAisberg, Eugeni
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Pred. No. 3.6e-47;
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                                                                                                                                       and methods of producing human kinesins
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                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 6
                                                                                                                                           Matches
                                                                                                                                                           Query Match
Best Local
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CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/295,612
PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: US 09/314,464
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TITLE OF INVENTION: No. 6331424el motor proteins
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                    LENGTH: 362
TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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     TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY 122
                                                             RICVCVRKRPLNKQELAKKEIDVISIPSKCLLLVHEPKLKVDLTKYLENQAFCFDFAFDE
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S 밁 8 밁 Ş 밁 á В δ В δ В á

Conservative

65;

10.9%;

Score 745.5; DB 4; Pred. No. 3.2e-47; 5; Mismatches 116;

Length

19;

Gaps

62

for Windows Version

1999-05-18

and

methods

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; ORGANISM: Human US-09-595-684B-33
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LENGTH:
                        GENERAL INFORMATION:
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Best Local Similarity 41.9
Matches 173; Conservative
                                            Sequence 6, Application US/09594669 Patent No. 6331424
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                                                                                                                                                                                                                                   359 GSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPRE
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Beraud, Christophe
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41.9%; Pred. No. 3.6e-47;
tive 76; Mismatches 143;
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RESULT 15
US-09-594-669-4
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; ORGANISM: Human
US-09-594-669-4
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Best Local Similarity
Matches 168; Conserv
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SEQ ID NO 4
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APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6331424el motor proteins
TITLE OF INVENTION: their use
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CURRENT FILING DATE: 2000-66-15
PRIOR APPLICATION NUMBER: US 09/295,612
PRIOR FILING DATE: 1999-04-20
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Pred. No. 3.5e-47;
5; Mismatches 116;
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                                                                                                                          RESULT 17
US-09-595-684B-25
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; NUMBER OF SEQ ID NOS:
; SOFTWARE: FastSEQ for
; SEQ ID NO 2
; LENGTH: 430
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US-09-594-669-2
                                                                     Sequence 25, Application US/09595684B Patent No. 6544766 GENERAL INFORMATION:
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APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: VAisberg, Eugeni
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APPLICANT: Sakowicz, Rom
TITLE OF INVENTION: No.
TITLE OF INVENTION: thei
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PRIOR FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: US 09/314,464
PRIOR FILING DATE: 1999-05-18
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CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 2000-06-15
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Pred. No. 4e-47;
5; Mismatches 1:
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; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-25
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US-09-724-510-2
                                                                                                                                                                                                                                                                           Sequence 2, Application US/097;
Patent No. 6432659
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITTE OF TAMENTION: NO. 643261
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Best Local Similarity
Matches 166; Conserv
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LENGTH: 678
                                                                                  NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 319
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CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                          APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6432659el motor proteins
TITLE OF INVENTION: their use
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TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: and purifying human kinesins
                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/724,510
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/675,227
PRIOR FILING DATE: 2000-09-29
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                                                                                                                                                                                                                               FILE REFERENCE: 1032
                                                     TYPE: PRT
ORGANISM: Human
   FEATURE:
NAME/KEY: VARIANT
LOCATION: (154)...
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(154)...(183)
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SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PAT
; ORGANISM: Human
FEATURE:
NAME/KEY: VARIANT
; LOCATION: (154)...(183)
; OTHER INFORMATION: Xaa = any amino acid
US-09-723-216-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Xaa = any amino US-09-724-510-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6436666el motor proteins
TITLE OF INVENTION: their use
FILE REFERENCE: 1032
                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 149
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Patent No. 6436686
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Best Local Similarity
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115
                                  124
                                                                                                                                                                                                                                  tch . 10.2%; Score 696.5; DB 4; al Similarity 45.8%; Pred. No. 1.1e-43; 149; Conservative 51; Mismatches 118;
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                                                                        61 ACTNODVYMKTTHPLIQHIF-NGGNATCFAYGOTGAGKTYTMIGTH-----ENPGLYALA 114
                                                                                                                 64
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                                                                                            TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA 123
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AKDIFRQLEVSQPRKHLFVWISFYEIYCGQLYDLLNRRKXXXXXXXXXXXXXXXXXXXXXX
                    AGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILR 183
                                                                                                                                                        KIRVCVRKRPLGMREVRRGEINIITVEDKETLLVHEKKEAVDLTQYILQHVFYFDEVFGE
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Pred. No. 1.1e-43;
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; LOCATION: (154)...(183)
; OTHER INFORMATION: Xaa =
US-09-675-227-2
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US-09-675-227-2
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SEQ ID NO 2
LENGTH: 319
               Sequence 4, Application Patent No. 6582958 GENERAL INFORMATION:
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TITLE OF INVENTION: No. 6461855el motor proteins and methods for
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 1032
CURRENT APPLICATION NUMBER: US/09/675,227
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 2
APPLICANT:
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       61 ACTNQDVYMKTTHPLIQHIF-NGGNATCFAYGQTGAGKTYTMIGTH-----ENPGLYALA
                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                VLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGS
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                                                                                                                                                                                                                                ERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKS
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                                                                                                                                  KTCMIANISPSHVATEHTLNTLRYA 318
                                                                                                                                                               KSIMIANISPTISCCEQTLUTLRYS 328
                                                                                                                                                                                                   ERAADARDSDROTKMEGAEINQSLLALKECIRALDQEHTHTPFRQSKLTQVLKDSFIGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIRVCVRKRPLGMREVRRGEINIITVEDKETLLVHEKKEAVDLTQYILQHVFYFDEVFGE
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Beraud, Christophe
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                                                 US/09722129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 696.5; DB 4;
Pred. No. 1.1e-43;
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US-09-722-129-2
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SEQ ID NO 2
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TITLE OF INVENTION: their use
FILE REFERENCE: 1054
CURRENT APPLICATION NUMBER: US/09/722,129
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09722129 Patent No. 6582958
                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Beraud, Chris
APPLICANT: Freedman, Ric
TITLE OF INVENTION: NO.
TITLE OF INVENTION: thei
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NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 1054
CURRENT APPLICATION NUMBER: US/09/722,129
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TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                  LENGTH: 492
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                                                  193 RÍCVCVRKRPLNQRÉTTLKÓLÓIÍTVPSDNVVMVHÉSKQKVÓLTRYLQNQTFCFÓHAFÓÓ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDL
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                   64
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TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY 122
                                                                     KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
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43.6%;
                                                                                                                                                                                                                                                                                                                                                                       Richard
No. 6582958el motor proteins
                                                                                                                                  8.6%;
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                                                                                                                   Score 589.5; DB 4;
pred. No. 1.7e-35;
6; Mismatches 108;
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Pred. No. 8.4e-36;
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APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION UMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1111
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US-09-914-259-28
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; ORGANISM: Saccharomyces cerevisiae
US-09-914-259-28
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SSIENVVIKSNHILLSNNNNNKINRGKIN--DKIERNNILKN------KSFDKPREGF 413
                                                                                                                          SLIALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTL
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                                                       EYATRAKSIKNTPQVNQSLSKDTCLKDYIQEIEKLRNDLKNSRNKQGIFITQ---DQLDL 458
                                                                                                                                                                                                                                   HAILNI-----DLKD--INKN-TSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINR
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                                                                                                                          CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ FOr Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 1073
TYPE: PRT
ORGANISM: S.pombe
US-09-541-782-6
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal
FILE REFERENCE: 1015
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 24
US-09-541-782-6
; Sequence 6, Application US/09541782
; Patent No. 6284480
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3; Mismatches 410;
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SKRELPATPSWTRDSSLIKETTNIN--LDSDKKFVRETYTSSNQTNEPDVYDK 1051
                                                   RKNNTNINSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNK 1010
                                                                                                                                                                                                           EVQTLDRLLQKVKEHSEDNTKEKHQQLLDLLESLVGNNDN------LIDSIKTP
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                                                                                                       HTELQKITDHVLKGTTSLANHTNELLGLGDESLCNLETTIEDTSLVK-----LETTGDTP 1000
                                                                                                                                                       EMKNNEMKDNEMKDNHIKSNNNNS--SSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIR
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US-09-723-820-6
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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Best Local Similarity
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APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
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TYPE: PRT
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  IKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKMEDNTPK 619
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                                                   SMEELLNTHSNQL---LISMTKITEHFQSLDEALQSARSSCAVPNS--SLDLIVSELKD-
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APPLICANT: Long, David M.
APPLICANT: Metz, Anneke M.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TE
FILE REFERENCE: 47714-5009-US
CURRENT APPLICATION NUMBER: US/09/417,485D
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 2184
TYPE: PRT
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US-09-417-485D-6
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Best Local S
Matches 330
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NAME/KEY: unsure
LOCATION: (330)..(335)

OTHER INFORMATION: Xaa at position
OTHER INFORMATION: Xaa at position
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                  KNYDFLSFSF---
                                                  NGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFI 144
                                                                                    NVINTKFGKIYRKFFPRKHILNKIHKIFKIIRLQIIKKYRIINIRMNRKFİKQKVYDTFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NIF-FDAISCDNWMYPNITNNNNNNN------NNNNNNNNNNIDVENYNNRDGTNNSMKLY 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNNNNNSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSS 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREGFTSTFGKYSSLND------IDKIK-----KNKKK---GLINYKSTLYND 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNKKLKKRNEPKMDYVQNMFNVKKKG------EKIKTNKYIF-IKKMKKKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDSELTK-----VLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSINNSNMISNSIYKSNYNSNQSISDVQI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRNFMLK----LNSINHFISKKLRI-NWIPKKKG----LRPLINLSTLNVPEIVKQRIFE 1120
                                                                       INSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNNVDNNN
                                                                                                           GNTQNKEKHDIYIGPIYNNSFDSTT----TTHSSNNY---KGNNIHVSGD-YKNDGLLHK 1505
                                                                                                                                               SUMNISSSSSSONNIYUNINDDDTFQUDYCHUDUTFTIRRKUUTUIUSUIYQUDDIIYT
                                                                                                                                                                                  RDKKRVENIKKWYLNSMKKINHDEILESLKNSSININN-----KNFMICTNHEQDTEEK
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                                       --SMNE-CYVKDIK------CNNNNNNNNNNNN
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Qy 221IDLKD-INKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANI 263	Oy 189 ELILKMIDGVLLRKIGVNSQNDESSRSHAILN	Query Match 7.8%; Score 533.5; DB 2; Length 2391; Best Local Similarity 20.4%; Pred. No. 2.1e-30; Matches 272; Conservative 225; Mismatches 404; Indels 431; Gaps 57;	; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-446-855A-2	Sin	H: CH	; REFERENCE/DOCKET NUMBER: 47-80 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 703-816-4000 ; TELEFAX: 703-816-4100	ATTORNEY/AGENT INFORMATION:  NAME: Mitchard, Leonard C  REGISTRATION NUMBER: 29.009	LICATION DATA: ON NUMBER: US/08/446, TE: 06-Jul-1995	; MEDIUM TIPE: FLODBY GISK ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARF: Datentin Peleace #1 24	8 5	Arlington Virginia : USA	; NUMBER OF SEQUENCES: 2 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Nixon & Vanderhye PC ; STREET: 1100 No. 5849573th Globe Road. 8th Floor	; APPLICANT: O'Sullivan, William J ; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl ; TITLE OF INVENTION: phosphate synthetase II	()()	; Sequence 2, Application US/08446855A ; Patent No. 5849573 ; GENERAL INFORMATION:	RESULT 27 US-08-446-855A-2	Db 1708 KKYKIKNKKKIQ-SVRNKRIHNQLVNANKK 1736	Qy 1252 SVLLNVSSNNGDIILLNKKLVQDNIKNSMDHNNIHKK 1288	QY 1203 DDQFHFYAYSRLEKDII-NLIMLRQIWCESENLRLLYQFLVVEYQNKSAN 1251	FLANG	1373 1154 T	LEEIDK	Db 1532 NNNINNSYNKLNCVTNNSKNDIIKYHKTIDTDNSKNHTYFK 1572
Db 1924 KFIYNFENSNGVIIAFGGQTSNNLVFSLYKNNV 1956	1007	1046 DNNNVDNNVDNNVDNVDNNVDNDD-DDVDFHNIKNENNNB	Db 1761 NTDEYDDDYYYDEDEEDDYDDDDDDDDDD	QY 991 HFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNNVDNNKUNVDNNV 1045	Qy 932 NIYNNINDDDTFQNDYCHND-NTFTIRRKNNTNINSNIYQNDDIIYTINSLNDYMSNTLL 990   ::	Qy 872 NNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSSSSSSSNN 931	Db 1603 MNCSNYNNASAFYNGKDRNDNLENDCIEKNMDHTYKHYNRLNNRRSTNERWMLMVN 1658	11 NORMALIA INGINAL KE DANKKISA KURINIA NA WEGINAN INGINALIA INGINALIA NA KURINIA NA WEGINAN INGINALIA NA KURINIA NA WEGINAN INGINALIA NA KURINIA NA	1487 KDMDGKNINDECKTYKKNKYKDMGLNNNIVDELSNGTSHSTNDHLYLDNFNTSDEEIGNN	720	Qy 660 NNGVINIINNSNVNSINNSNWNSINNSNWNSNSIYKSNYNSNQSISDVQIRYVNEMDTSN 719	QY 600 NKDNTFFKSNINKMEDNTPKDILYESRNVSNYNGNVLLGLNKNTHHDISTKDENHNDNKI 659   :    :    :  :  :  :  :  :  :  :  :  :	н	540 CHLNNNDKSIFLHKKNIRDNIKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMF	Qy 480 SSMVNNMINHMINNNINNVNNNNNNNNNNNNNHNHLPQPNYAFTDTSDFSSLDDMN 539	Db 1272 KVHVKNHLYNEVVDDKDTQLHKENNNNNNMNSGNVENKCKLNKESYGYNNSSNCINTNNI 1331	RKK	414 TSTFGKYSSLNDIDKI	Db 1170 FKKHGFSDKQIAHYLSFNTSDNNNNNNNISSCRVTENDVMKY 1211	1116 AIHÓAFHLNMPMDKIHELTHIDYWFLHKFYNIYNLQNKLKTLKLÉQLSFNDLKY	QY 317 CCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSKG 359	Db 1068 GRTFEESIQKSURCIDDNYLGFSNTYCIDWDEKKIIEBLKNPSPKRID 1115	1008 ALGYDLISLKNSITKKTTACFEPSLDYITTKIPRWDLNKFEFASNTMNSSMKSVGEVMSI

Qy  414 TSTFGKYSSLNDIDKIKKNKKKG 436	Db 1116 AIHQAFHLNNPMDKIHELTHIDYWFLHKFYNIYNLQNKLKTLKLEQUSFNDLKY 1169  Qy 360 SEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPREGF 413  Qy :	317 CCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSKG	264 NRSL-LALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKSKSIMIANISP-TIS 	221IDLKD-INKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANI 	Qy 189 ELILKMIDGVLLRKIGVNSQNDESSRSHAILN 220 	Query Match 7.8%; Score 533.5; DB 3; Length 2391; Best Local Similarity 20.4%; Pred. No. 2.1e-30; Matches 272; Conservative 225; Mismatches 404; Indels 431; Gaps 57;	; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: protein US-09-150-741-2	PatentIn Ver	FILING DATE: 1993-1: APPLICATION NUMBER: FILING DATE: 1995-0 F SEO ID NOS: 15	CURRENT FILING DATE: 1998-09-10 ; CURRENT FILING DATE: 1998-09-10 ; EARLIER APPLICATION NUMBER: PL6380 ; EARLIER FILING DATE: 1992-12-16 ; EARLIER APPLICATION NUMBER: A103/0617	NO. 6183996 OF INVENTION: Synthetase II REFERENCE:	Patent No. 618396  Patent No. 618396  GENERAL INFORMATION:  APPLICANT: Stewart et al.  TITUE DE INVENTION: Nucleotide Semience Encoding Carbamovi Dhogabate	RESULT 28 US-09-150-741-2 • Semience 2 Application US/09150741	Qy 1272 VQDNIKNSMDHN 1283 : :::: :  : Db 2074 ISEHVENAGVHS 2085	OY 1220 NLIMLRQIWCESENLRLLYQFLVVEYQNKSANSVLLNVSSNNGDIILLNKKL 1271 :	QY 1183 NETSDLYKDLVMCHICNNNPDDQFHFYAYSRLEKDII 1219
RESULT 29 US-09-914-259-21 US-09-914-259-21 ; Sequence 21, Application US/09914259 ; Patent No. 6495336 ; GENERAL INFORMATION: ; APPLICANT: Makowski, Lee ; APPLICANT: Hyman, Paul	Qy 1272 VQDNIKNSMDHN 1283 : ::::  :  : Db 2074 ISEHVENAGVHS 2085	Qy 1220 NLIMLRQIWCESENLRLLYQFLVVEYQNKGANSVLLNVSSNNGDIILLNKKL 1271  ; ;       ;     ;   ;   ;	AYSRLEKDII :::          KFTKLSKAIQFANEVKFPVLVRPSYVL	1124 LSKYKABKON-VIKKYINEDIKNMSLEEIDKTAQSIYEKRKVLLTKLLLIFKKNVDTQIN  1924 KFIYNFENSNGVIIAFGGQTSNNLVFSLYKNNV	Db 1865 GCYRIGSSVEFDWSAIHCVKTIRKLNHKAILING-NPETVSTDYDESDRLYFDEITTEVI 1923	1046 DMNVUDNIVDANDKANVUDANNEVDRUDG-DVUFRINTAVERNINGE	991 HKEKTIYPTISTINEDIYNKEMEGKHIKLDDQKXIDIRUMWWWWWWAKWAVWODNN 	<u></u>	Qy 872 NNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKONEMKDNHIKSNNNNSSSSSSSNN 931   : :	Qy 813 MMFCHYNLNDKNYLIDLNNKEQKDKNIHGC-DNNIIQNRNDFEKKKKTNFYNNNNIVIVN 871	Qy 771 NSMKLYAYNSHNLFQPDNNKNTSNQNINTNKN-NQDGNVNYS 812	Qy 720 KNNDNIFFDAISCDNNMYFNITHNNNNNNNNNNNNNNNNIDVENYNNRDGTN 770	Qy 660 NNGVINIINNSNVNSINNSNVNSNSIYKSNYNSNQSISDVQIRYVNEMDTSN 719	Qy 600 NKDNTFFKSNINKMEDNTPKDILYESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKI 659		480 SSMVNNMINHMINNNINNNINNNNNNNNNNNNNNHLPQPNYAFTDTSDFSSLDDMN : :           : :     :

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; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 967
; TYPE: PAT
; ORGANISM: Loligo pealeii
US-09-914-259-21
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Best Local Similarity
Matches 217; Conserv
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E-QHQKQLQSLRDEISEKQATVDNLKD-DNQRLSLALEKLQA--DYDKLKQEEVEKAAKL
                             NITHNINNINNINNINNINNI DVENYNNRDGTNISM---KLYAYISHILFQPDNIKNTSII
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                                                                                           INNSNMNSNSIYKSNYNSNQSISDVQIRYV----NEMDTSNKNNDNIFFDAISCDNNMYP
                                                                                                                                                                                          KDLGDIGTIVG---GNAAETKPTAGS-----GEKIEEEFTVARLYISKMKS-----
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                                                                                                                          -EVKTLVSRNNQL-----ENTQQDNFKKIETHEKDLSNCKLLIQQHEAKMASLQEAIKDS
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; LENGTH: 1184
; TYPE: PRT
; ORGANISM: A. nidulans
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US-09-541-782-2
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Best Local Sim
Matches 253;
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APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09541782 Patent No. 6284480
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CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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VLQNTRAQLEEEEMLRCAHEETEHQLQDVGKGLISTLGQTVEDINSLQSK---
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218 ILNIDLKDINKNTSL------GKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLAL
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Similarity 21.1%; Pred. No. 2.4e-28;
53; Conservative 194; Mismatches 415;
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                                                       RRIISEEQRAKIESMESSLRHKVQELLTLTSK-FNDLKKDNDDTLAALCSTNDVLQQTDI
                                                                                                              NHLLSNNNNNKIN--RGKINDKIERNNILKNKSFDKPREGFTSTFGKYSSLNDI----DK 428
                                                                                                                                                                  AKNIRNKPQ-INSTMPKMTLLREFTAEIEKLKAELIATRHRNGVYMSVESYEEMKMENES
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961 NTNINSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIXNKE 1011 	2 NSKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDM-TKYIERHEE
UNLIKSNNNNSSSSSSNNNI ININDUDITE QNUI CHWURIE IIR	Query Match 7.3%; Score 500; DB 4; Length 1184;  Best Local Similarity 21.1%; Pred. No. 2.4e-28;  Matches 253; Conservative 194; Mismatches 415; Indels 338; Gaps 48;
KKKTNFYNNNNIVIVNNNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKD :	LENGTH: 1184 .  TYPE: PRT ORGANISM: A. nidulans S-09-723-820-2
796 QNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLNNKEQKDKNIHGCDNNIIQNRNDFEK 855 	<b>.</b>
	REFERENCE: 1015 NT APPLICATION NUMBER: US/ NT FILING DATE: 2000-11-2 APPLICATION NUMBER: 09/54
684 NNSNMNSNYKSNYNSNQSISDVQIRYVNEMDTSNKNNDNIFFDAISCDNN 735 	
624 ESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKINNGVINIINNSNVNSINNSNMNSI 683	US-09-723-820-2  y Sequence 2, Application US/09723820  parent No. 6468760  CENERAL INFORMATION:  Db
TFFKSNINKMEDNTPKDILY	Db 1037 MEVLPFNSDDQLSGPSSSPGGSPSKGFVYNDVEDEVGTHAPTVTNVNDKNIVDANV 1096 Qy
505 NNNNNNNNNNHNHLFQP-NYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLK 563	985 LTDLSSS-FQNRSLEEYVATGVTPKKRKYDYISVLPSTESHEVLKSRLRTTKE 1036
OTRHAKLLETTSVKVNEFIATEISN	NTNINSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKE
531 VLQNTRAQLEEEEMLRCAHEETEHQLQDVGKGLISTLGQTVEDINSLQSKLD 582	913 DNHIKSNNNNNSSSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTTRRKN 960
375 NHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPREGFTSTFGKYSSLNDIDK 428	Db 853 KDVNASKD
413 AKNIRNKPQ-INSTMPKMTLLREFTABIEKLKABLIATRHRNGVYMSVESYEEMKMENES 471	OD 829 MLEQAI:
353 GRVINALUDKSQHIPYRESKLTRLLQDSLGGRTKTCIIATMSPARSNLEETISTLDYAFR 412	736 MYPNITNNNNNNNNNNNNNNNNNNNNNNNNDGTNNSMKLYAYNSHNLEQPDNNKNTSNI 795
	Db 769 HKASAHLAQAIEEEHVAAEAEREILMSQIKALVEESRQKQFARLRAKIDGVRTEISASGD 828 Qy
218 ILNIDLKDINKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLAL 270	733
247 GHMSTLVQGMEETYIDSATAGIKLLQQGSHKRQVAATKCNDLSSRSHT 294	624 ESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKINNGVINIINNSNVNSINNSNMNSI 683
189 SDNAGIIPRVLYSLFAKLADTESTVKCSFIELYNEELRDLLSAEENPKLKIYDNEQKK 246 162 KMVAALENGKKEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHA 217	Qy 564 NRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKMEDNTPKDILY 623 Db :       : :     : :     : :     : :     : :     : :     : :     : :     : :     : :     : :     : :     : :     : :     : : :     : : :     : : :     : : :   : :   : :   : :   : : :   : : :   : : :   : : :   : : : :   : : : :   : : : :   : : : :   : : : : :   : : : : :   : : : : :   : : : : : : : :   :
QYAAGDIPTFLNIYDKDNTKGIFISFYBIYCGKLYDLLQKR	642 IERTRSDLSEYNRSLDAACNNAKAETSSAHEDMVNVLEEIKDLREEVKSK 691
61 FDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIF 120	
	Qy 464 NNDNNNNNNNDSSSMVNNMINHMINNNINNNINVNNN 504 Db

229NTSLGKIAFIDLAGSERADTYSQNKQTQTDGANINRSLLALKECIRAMDSDKN  :	Qy  5 IKVVVRKRPLSELEKKKKDSDIITVKONCTLYIDEPRYKVDMTKYIERHEF 55  1	CURRENT APPLICATION NUMBER: US/09/595,684B CURRENT APPLICATION NUMBER: US/09/595,684B CURRENT FILING DATE: 2002-06-24 PRIOR APPLICATION NUMBER: 09/295,612 PRIOR FILING DATE: 2000-04-20 NUMBER OF SEQ ID NOS: 105 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 31 LENGTH: 2662 TYPE: PRT ORGANISM: Human US-09-595-684B-31 Ouery Match Best Local Similarity 18.7%; Pred. No. 1.6e-26; Matches 305; Conservative 263; Mismatches 607; Indels 458; Gaps 59;	US-09-595-684B-31  Sequence 31, Application US/09595684B  Patent No. 6544766  Patent No. 6544766  GENERAL INFORMATION:  APPLICANT: Beraud, Christophe APPLICANT: Ohashi, Cara APPLICANT: Sakowicz, Roman  APPLICANT: Waisberg, Eugeni APPLICANT: Wood, Kenneth APPLICANT: Yu, Ming TITLE OF INVENTION: and purifying human kinesins	Qy 1012 MEGKHIRLDDQDKYDDNDNNNVDNNVKNNVDNNV 1045
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1065 -NNVDNDDDDVDFHNIKNFNNNEYLSYFQKNVDTIINNCLNSLDISSMY 1112 1122 IREIEATGLQTKEELKIAHHLKEHQETIDELRRSVSEKTAQIINTQDLEKSHTKLQEEI 1281 1113		673 NSINNSNMMSINNSNMMSNIYKSNYNSNQSISDVQIRYVNEMDTSNKNNDNIFFDA 729  805 LATTQSNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQBIVNLSKEA 854  730 ISCDNNM	571 QDLENELSSKVELLREKEDQIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDA 630 538 MNCHLNNNDKSIFLHKKNLRDNIKLKNRSSCDNIMNKKKONLHLARHSVGSKLTMFSYDP 597	.  511 VLDYEQLRTEKEĖMELKLKEKNDLDEFEALERKTKKDQEMQLIHEISNLKNLVKHREVYN 570  491INNININININVNNNNNNNNNNNNNHLPQPNYAFTDTSDFSSLDD 537  ;   ::: : : : : : : : : : : : : : : : :

367; 35;

Gaps

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364 336 126

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APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6492151el motor proteins and
TITLE OF INVENTION: their use
FILE REFERENCE: 1046
CURRENT APPLICATION NUMBER: US/09/723,097
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/632,344
PRIOR APPLICATION NUMBER: 09/632,344
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 367
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US-09-724-511-2
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US-09-723-097-2
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
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Best Local
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TITLE OF INVENTION: No. 6391601el motor proteins and methods for
TITLE OF INVENTION: their use
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CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/632,344
PRIOR FILING DATE: 2000-08-03
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SOFTWARE: FastSEQ for Windows Version
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similarity 33.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKEVEDAVEDETSTQSEVEEHTTKP-ILRSFLNGYNCTVLAYGATGAGKTHTMLGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKVVVRVRPENTKEKAAGFHKVVHVVDKHILVFDPKQEEVSFFHGKKTTNQNVIKKQNKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NONVRIAKMSLIDLAGSER-ASTSGAKGTRFVEGTNINRSLLALGNVINALADSKISFLC
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Pred. No. 1.6e-26;
6; Mismatches 137;
                                                                                                                                                                                                                                                                                         and methods
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Best Local Similarity
Matches 122; Conserv
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09632344 Patent No. 6534309
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Matches 122;
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Best Local
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TITLE OF INVENTION:
FILE REFERENCE: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/632,344
CURRENT FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6534309el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 367
TYPE: PRT
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  227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLK-----DI
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                                                                                                                                                                                                       QSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKWVAALENGKK 172
                                                                                                                                                                                                                                                              FastSEQ for Windows Version
NKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDK-----
                                                      GVVVHGLTLHQPKSSEEILHLLDNGNKNRTQHPTDMNATSSRSHAVFQIYLRQQDKTASI
                                                                                                     EVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLK-----DI
                                                                                                                                                         -ADEPGVMYLTMLHLYKCMDEIKEEKICSTAVSYLEVÝNEQIRDLLVNSGPLÁVREDTQK 185
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Pred. No. 1.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 465.5; DB 4;
Pred. No. 1.6e-26;
6; Mismatches 137;
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RESULT 36
US-09-541-782-4
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SEQ ID NO 4
LENGTH: 1038
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Nislow, Corey
APPLICANT: Sakwaicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09541782 Patent No. 6284480
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Best Local
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CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
    476
                                             564
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                                                                                    423
                                                                                                                                                                363 NASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPREGFTSTFGKYSS
                                                                                                                                                                                                                                                                                                                                                                            365 TNAMEGLNLLOKGLKHROVASTKMNDFSSRSHTIFTITLYKKHODELFRISKMNLVDLAG
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                                                                                                                                                                                                                                                                                                                    SERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSBLTKVLRDIFVGK
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  NNDSSSMVNNMINHM----INNNINNNINNNNNNNNNNNNSHNNHLPQPNYAFTDTSDF
                                                                                LN-DIDKIK-----KNKKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNNNNNNN
                                                                                                                           GSFIMKDILVK---
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                                         LNSDLESYKNEVQECKREIESLISKNALLVKDKLKSKETIQSQNCQIES---
                                                                                                                                                                                                            TKTALIATISPAKVTSEETCSTLEYASKAKNIKNK-----
                                                                                                                                                                                                                                                                                          SENINRSGALNQRAKEAG-SINQSLLTLGRVINALVDKSGHIPFRESKLTRLLQDSLGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQQYQQQQAVNSRNNSSSNSGSTTNNASSNTNTNNGQRSSMAPNDQTNGIYIQNLQEFHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NHIPFRDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 172; Mismatches 366;
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                                                                                                                           ---NITMELAKI-----KSDLLSTKS----KEGIYMSQDHYKN
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Pred. No. 7.5e-26;
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                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/541,782
PRIOR FLIING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 4
LENGTH: 1038
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-723-820-4
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                                                                                    Matches
                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/723,
CURRENT FILING DATE: 200-11-28
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                                                                                  246;
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ITVAVRCRGRNEREISMKSSVVVNVPDITGSKEISINTT------GDTGITAQMNAKRY 127
                                    IKVVVRKRPLSELEKKKKDSDIITVKN-----NCTLYIDEPRYKVDMTKYIERHEF
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                                                                              6.8%; Score 465; DB 4; ilarity 20.2%; Pred. No. 7.5e-26; Conservative 172; Mismatches 366;
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CURRENT APPLICATION NUMBER: US/09/723,
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/632,344
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US-09-724-511-4
                                                                                                                                                                US-09-723-097-4
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6492151e1
TITLE OF INVENTION: their use
FILE REFERENCE: 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/724,511
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/632,344
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                         Sequence 4, Application Patent No. 6492151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
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APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6391601el motor proteins
TITLE OF INVENTION: their use
FILE REFERENCE: 1046
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Similarity 34.0%;
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                                             motor proteins
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CURRENT APPLICATION NUMBER: US/09/632,344
CURRENT FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 355
TYPE: PRT
ORGANISM: Human
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; ORGANISM: Human
US-09-723-097-4
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Patent No. 6534309
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6534309el motor proteins and methods for
TITLE OF INVENTION: their use
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 4
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                                                                             64 LKFVFDAVFDETSTQSEVFEHTTKP-ILRSFLNGYNCTVLAYGATGAGKTHTMLGS---- 118
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                                                                                                           HEFIVDKVFDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYG 112
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                     QSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKK 172
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-ADEPGVMYLTMLHLYKCMDEIKEEKICSTAVSYLEVYNEQIRDLLVNSGPLAVREDTOK
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                                                                                                                                                                                                                                     6.8%; Score 464.5; DB 4; Length 355; 34.0%; Pred. No. 1.8e-26; tive 65; Mismatches 137; Indels 35
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Search completed: October 2, 2003, 16:28:17 Job time: 44 secs

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Result
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pria and is derived by analysis of the total score distribution.
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1 MNSKIKVVVRKRPL
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US-10-159-151-10
US-10-159-151-2
US-10-159-151-2
US-10-159-151-4
US-09-849-602-20
US-09-723-276-2
US-09-820-843A-106
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Sequence 4, Appli
Sequence 20, Appli
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Sequence 108, App
Sequence 109, App
Sequence 17, Appli
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## ALIGNMENT

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Sequence 2, Application US/10006780

Publication No. US20030104496A1

GENERAL INFORMATION:
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
APPLICANT: Guo, Jun
APPLICANT: Freedman, Richard
TITLE OF INVENTION: NOVEL MOTOR PROTEIN OF P.
TITLE OF INVENTION: METHODS FOR ITS USE
FILE REFERENCE: CYTOP083

CURRENT APPLICATION NUMBER: US/10/006,780

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1288
TYPEE: PRT
COGGANISM: Plasmodium falciparum
US-10-006-780-2
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                                                                                                                                                                    1 MNSKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKV
                                                                         FDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIF
                      QYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK
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                                                NPDDQFHFYAYSRLEKDIINLIMLRQIWCESENLRLLYQFLVVEYQNKSANSVLLNVSSN
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Sequence 10, Application US/10006780

Publication No. US20030104496A1

GENERAL INFORMATION:

APPLICANT: Sakowicz, Roman

APPLICANT: Beraud, Christophe

APPLICANT: Freedman, Richard

APPLICANT: Freedman, Richard

TITLE OF INVENTION: MOVEL MOTOR PROTEIN OF P

TITLE OF INVENTION: METHODS FOR ITS USE

FILE REFERENCE: CTOTOP083

CURRENT APPLICATION UMMER: US/10/006,780

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 332
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CURRENT APPLICATION NUMBER: US/10/006,780
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 355
TYPE: PRT
ORGANISM: P. Falciparum
US-10-006-780-6
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APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
APPLICANT: Guo, Jun
APPLICANT: Freedman, Richard
TITLE OF INVENTION: NOVEL MOTOR PROTEIN OF
TITLE OF INVENTION: METHODS FOR ITS USE
FILE REFERENCE: CYTOP083
RESULT 3
US-10-006-780-10
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Similarity 100.0%;
54; Conservative 0;
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Sequence 4, Application US/10006780
Publication No. US20030104496A1
GENERAL INFORMATION:
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
APPLICANT: Guo, Jun
APPLICANT: Guo, Jun
APPLICANT: Guo, Jun
APPLICANT: Guo, Jun
TITLE OF INVENTION: MOVEL MOTOR PROTEIN OF P.
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; ORGANISM: P.
US-10-006-780-10
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                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CYTOP083
CURRENT APPLICATION NUMBER: US/10/006,780
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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Best Local (
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                                                               AGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILR 183
                                                                                                       TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA
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VLTKEBLILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGS
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                                              AGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILR
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; Sequence 10, Application US/10159151
; Publication No. US20030036075A1
; GENERAL INFORMATION:
; APPLICANT: Cytokinetics, Inc.
; APPLICANT: Beraud, Christopher
; APPLICANT: Guo, Jun
; APPLICANT: Freedman, Richard
; APPLICANT: Patel, Umesh A.
; APPLICANT: Davies, Katherine A.

Guo, Jun Freedman, Richard Patel, Umesh A. Davies, Katherine A

RESULT 6 US-10-159-151-10

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CURRENT APPLICATION NUMBER: US/10/006,780
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 361
TYPE: PRT
ORGANISM: P. Falciparum
US-10-006-780-8
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APPLICANT: Beraud, Christophe
APPLICANT: Guo, Jun
APPLICANT: Guo, Jun
TITLE OF INVENTION: MOYOR PROTEIN OF
TITLE OF INVENTION: METHODS FOR ITS USE
FILE REFERENCE: CYTOP083
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Local Similarity 99.4%;
les 331; Conservative
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KSIMIANISPTISCCEQTLNTLRYSSRVKNFKN 336
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Pred. No. 2.7e-111;
0; Mismatches 2;
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-159-151-10
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Best Local
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                                      SEQ ID NO 6
LENGTH: 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/675,227
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 10
                                                                                                                      PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/675,227
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                      FILE REFERENCE: 020552-002400US
CURRENT APPLICATION NUMBER: US/10/159,151
CURRENT FILING DATE: 2002-05-31
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cytokinetics, APPLICANT: Beraud, Chri APPLICANT: Guo, Jun
                                                                               SOFTWARE: PatentIn Ver.
                                                                                                       NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/967,908
                                                                                                                                                                                                                                                                  APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: KINI-3 MOTOR PROTEIN AND METHODS
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTCMIANISPSHVATEHTLNTLRYADRVKELKKGIKCCTSVTSRN 349
                                                                                                                                                                                                                                                                                                                                   Freedman, Richard
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47.5%;
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Pred. No. 3.2e-46;
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OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: fragment V195-S566 with flanking vector sequence.
US-10-159-151-6
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Best Local
                                                                                                                     Best Local Similarity
Matches 164; Conserva
                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: KINI-3 MCTOR PROTEIN AND METHODS
FILE REFERENCE: 020552-002400US
CURRENT APPLICATION NUMBER: US/10/159,151
CURRENT FILING DATE: 2002-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cytokinetics, APPLICANT: Beraud, Chri APPLICANT: Guo, Jun
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/675,227 PRIOR FILING DATE: 2000-09-29 NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/967,908
PRIOR FILING DATE: 2001-09-28
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                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                       LENGTH: 1368
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64 TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA
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                                       KIRVCVRKRPLGMREVRRGEINÍÍÍÍVEDKETLLVHEKKEAVDLÍQÝÍLQHVFYFDEVFGE
                                                                             KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
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                                                                                                                                                                                                                      Description of Artificial Sequence: KinI-3 domain fragment
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                                                                                                                     11.2%; Score 768.5; DB 1
47.5%; Pred. No. 1.9e-45;
tive 58; Mismatches 116
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FILE REFERENCE: 020552-002400US
CURRENT APPLICATION NUMBER: US/10/159,151
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US/09/567,908
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/675,227
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN OB
SOFTWARE: PATENTIN OB
LENGTH: 343
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APPLICANT: Cytokinetics, Inc.
APPLICANT: Beraud, Christopher
APPLICANT: Guo, Jun
APPLICANT: Freedman, Richard
APPLICANT: Patel, Umesh A.
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 161; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: KINI-3 MOTOR PROTEIN AND METHODS FOR ITS USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: fragment E213-S546.
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                 ERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKWHIPFRDSELTKVLRDIFVGKS
                                                                 VDSVELLLEVILKGSKERSTGATGVNADSSRSHAVIQIQIKDSAKRT-FGRISFIDLAGS
                                                                                              VLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGS
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ERAADARDSDROTKMEGAEINOSLLALKECIRALDOEHTHTPFROSKLTQVLKDSFIGNA
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RESULT 11
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US-10-159-151-4
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CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US/09/967,908
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/675,227
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
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Best Local S
Matches 161
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LENGTH: 373
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fragment
OTHER INFORMATION: encoding residues D183-D546 with flanking vec
OTHER INFORMATION: sequence.
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APPLICANT: Beraud, Christopher
APPLICANT: Guo, Jun
APPLICANT: Freedman, Richard
APPLICANT: Patel, Umesh A.
APPLICANT: Davies, Katherine A.
APPLICANT: Davies, KXINI-3 MOTOR PROTEIN AND METHODS
FILE REFERENCE: 020552-002400US
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                                                                                                                                                                                                                                                        VLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGS
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                                                                                                          KSIMIANISPTISCCEQTLNTLRYSSRVK 332
                                                                           KTCMIANISPSHVATEHTLNTLRYADRVK 363
                                                                                                                                                      ERAADARDSDROTKMEGAEINQSLLALKECIRALDQEHTHTPFRQSKLTQVLKDSFIGNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 758.5; DB 1
48.9%; Pred. No. 1.7e-45;
tive 58; Mismatches 103
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Sequence 20, Application US/09849602
Publication No. US20030165834A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Old, Lloyd J.

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APPLICANT: Stockert, Elisaucu.
APPLICANT: Chen, Yao-Tseng
ITITLE OF INVENTION: Colon Cancer Antigen Pan.
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 725
TYPE: PAT
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-723-276-2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
:-09-849-602-20
                                                                                                    SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 319
TYPE: PRT
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                                                                                                                                                                                                                                                                    APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. US20020101952A1el motor
TITLE OF INVENTION: their use
OTHER INFORMATION: Xaa = -09-723-276-2
                                                                                                                                                                                                                         FILE REFERENCE: 1032
CURRENT APPLICATION NUMBER: US/09/723.
CURRENT FILING DATE: 2000-11-27
                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/675,227
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                             APPLICANT: Beraud, Christophe APPLICANT: Freedman, Richard
                                NAME/KEY: VARIANT LOCATION: (154)...(183)
                                                                                    ORGANISM: Human
                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEEMEACS -- NGALIPGNLSKEEEELSSQMSSFNEAMTQIRELEEKAMEELKE
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ilarity 41.9%;
Conservative 7
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N: Colon Cancer Antigen Panel
                any amino acid
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Pred. No. 1.5e-44;
6; Mismatches 143;
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RESULT 13
US-09-820-843A-108
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Publication No. US2003003963A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION OF CANDIDATE PROTE
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 807

TYPE: PRT
TYPE: PRT
ORGANISM: Plasmodium falciparum
FEATURE:
NAME KEY: misc feature
NAME/KEY: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: 91|3845292
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                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                  388 RGKINDKIERNNILKNKSFDKPREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYN-
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 178
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                                                                                                                                                                                                                                                                       h 10.2%; Score 696; DB 11; Similarity 26.6%; Pred. No. 1.2e-40; 53; Conservative 151; Mismatches 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTNODVYMKTTHPLIQHIF-NGGNATCFAYGQTGAGKTYTMIGTH-----ENPGLYALA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVDNETVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA 123
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                                                                                                                                                                                                                                         SSRVKNFKNKSTCINEEDDTNTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNNKIN
                               - NINI NVNNNNNNNNNNNNNNSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKK
                                                                                                                                    QEKNKKKKKKNTHKKVNINNTHINIHTTNDKNNG-QDINKPEVIERDNIINIKNDTNNI
                                                                                                                                                                                                        SSKEKNEEN--DIINKCDDSN-----KINGKE-NIFAVEKVGINESGHMSNDNINK-N
                                                                   LDSSYNEEGNENNRNDINNNNNNNNININNNNNSCSNNYGLKKKITLLKRNDIKDEGY
                                                                                                 Conservative
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45.8%; Pred. No. 3.2e-41;
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                                                                                                                                                                                                                                                                                                         Length 807;
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OTHER INFORMATI NAME/KEY: misc OTHER INFORMATI S-09-820-843A-109	; TYPE: PRT ; ORGANISM: Plasmodium falciparum ; FEATURE: ; NAME/KEY: misc_feature	е С	TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES FILE REFERENCE: Q63915 CURRENT APPLICATION NUMBER: US/09/820,843A CURRENT FILING DATE: 2001-03-30	Publica GENERAL APPLICA TITLE	RESULT 14 US-09-820-843A-109 ; Sequence 109, Application US/09820843A	Qy 1149 EEIDKTAQ-SIYEKRKVLLTKLLLLFKKNVDTQINNETSDL 1188	QY 1092 QKNVDTIINNCLNSLDISSMYDDTKBILNNILLSKYKAEKDNVIKKYINEDIKNMSL 1148	Qy 1057NGKUNVDNNVDNDDDDVDFHNIKNFNNNEYLSYF 1091	Qy 1007 IYNKEMEGKHIRLDDQDKYDDNDNNNVDNNVDNNVDDNNNVDNNVDN 1056	Qy 947 YCHNDNTETIRRKNNTNINSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYTYPTLSTNED 1006	Qy 889 SHTSIDMKNNEMKNNEMKDNEMKDNHIKSNNNNSSSSSSNNNIYNNINDDDTFQND 946	QY 834QKDKNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIVIVNNNMGNNNSPRMKYGLCG 888  L	Qy 776 YAYNSHNLFQPDNNKNTSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLID-LNNKE- 833	Qy 725 IFFDAISCDNNMYPNITNNNNNNNNNNNNNNNNDVENYNNRDGTNNSMKL 775	Qy 670 SNVNSINNSNMNSINNSNMNSNSIYKSNYNSNQSISDVQIRYVNEM-DTSNKNNDN 724	Qy 615 DNTPKDILYESRNVSNMIGNVLLGLNKNTHHDISTKDENHNDNKINNGVINIINN 669	QY 555 NLRDNIKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKME 614   ::    ::    ::    ::    ::
d Q	Db Qy	ДУ	Db Qy	Qу	Qу	Db od	Qу	Фу	ОУ	dg dg	οd da	D Qy	DЬ	D Qy	Qy da	B &	Query M Best Lo Matches
1270 K 1270     827 K 827	1210 AYSRLEKDIINLIMLRQIWCESENLRLLYQFLVVEYQNKSANSVLLNVSSNNGDIILLNK 1269	1150 EIDKTAGSIYEKRKVLLTKLLLLFKKOVDTQINNETSDLRKDLVMCHICNNNPDDQFHFY 1209	1090 YFQKNVDTIINNCLNSLDISSMYDDTKEILNNILLSKYKAEKDNVIKKYINEDIKNMSLE 1149 :	1041 VDNNVDNV-NVDNNVDNNDKNNVDNNVDNDDDDVDFHNIKNFNNNEYLS 1089	981 LNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNNVDNNNKNN 1040 	929SNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQNDDIIYTINS 980 	869 IVNNNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSSSSSS 928	813 MNFCHYNLNDKNYLIDLNNKEQKDKNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIV 868	753 NNNNNIDVENYNNRDGTNNSMKLYAYNSHNLFQPDNNKNTSNIQNINTNKNNQDGNVNYS 812	699 NSNQSISDVÓIRYVNEMDTSNKNNDNIFFDAISCDNNMYPNITNNNNNNNNNNN 752 	648 STKDENHNDNKINNGVINIINNSNVNSINNSNWNSINNSNMNSNSIYKSNY 698	616 NTPKD	569DNIMNKKKNNLHLARHSVGSKLTWFSYDDQKNKDNTFFKSNINKMED 615	512 NNSHNNHLPODNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSSC 568   :	453 KHNNNNNNNNNNNNNNNNNNNNNNNNNNNSSSMYNNMINHMINNNINNNNI-NVNNNNNNNNNNNN 511	393 DKIERNNILKNKSFDKPREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYNDNTINK 452   : : : : :   :   :   :   :   :   :	Query Match Best Local Similarity 26.4%; Pred. No. 1.6e-40; Matches 254; Conservative 145; Mismatches 325; Indels 237; Gaps 41;

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RESULT 15
US-10-135-322-17
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APPLICANT: HELARIUTTA, N
APPLICANT: HELARIUTTA, N
APPLICANT: MAHONEN, AP
APPLICANT: BONKE, AWM
APPLICANT: KAUPPINEN, L
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Best Local Similarity
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: 60/253,739
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 43
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APPLICANT: KAUPPITEN, L
APPLICANT: RIIKONEN, M
TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER
FILE REFERENCE: 5914-086-999
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TYPE: PRT
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                                   HIKSNYNNSSSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQ----
                                                                                                                                                                       NQDGNVNYSMNFCHYNLNDKNYLIDLNNKEQKDKNIHGCD-----NNIIQNRNDFE
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                                                                                          KKKKTNFYNNNNIVIVNNNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDN 914
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Pred. No. 1.1e-38;
6; Mismatches 255;
                                                                   GHCIQTISEEILGNKPVVYNNGNNN-----
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RESULT 16
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US-09-925-300-1074
                                            Query Match
Best Local S
Matches 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
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NAME/KEY: SITE
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TITLE OF INVENTION: Nucleic Acids, Proteins
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (177)
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                                            al Similarity
149; Conserv
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4 KIKVVVRKRPLSELEKKKKDSDIITVKUNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
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                                               59; Mismatches 102;
                                                            Score 672; DB 10;
Pred. No. 2.4e-39;
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RESULT 17  US-10-087-464-50  Sequence 50, Application US/10087464  Publication No. US20030059436A1  GENERAL INCORMATION: APPLICANT: Lii, Knerong TITLE OF INVENTON: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof. PRICAPT: Lii, Knerong TITLE OF INVENTON: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof. PRICA PPLICANT: Lii, Knerong TITLE OF INVENTON: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof. PRICA PPLICATION UNMERS: US 06/272,930  PRICA PPLICATION UNMERS: US 06/272,930  PRICA PRILIAGO DATE: 2002-03-01  PRICA PRILAGO DATE: 2002-03-02  INMERS OF SEO ID NOS: 59  SOPTWARE: Patentin version 3.0  PRICA PRILAGO DATE: 2002-03-02  INMERS OF SEO ID NOS: 59  SOPTWARE: Patentin version 3.0  LENGTH: 331; Conservative 180; Mismatches 412; Indels 512; Gaps 68;  DEST ID NOS 50  LENGTH: 331; Conservative 180; Mismatches 412; Indels 512; Gaps 68;  PRICA PRICAPTION OF THE PRICATION OF THE PRICAPT OF THE PRICAPTION OF THE PRICAPT OF THE PRI	Qy 300 VGK-SKSIMIANISPTISCC 318 : :  ::	Qy 240 LAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIF 299    :       ::  :	Qy 181 ILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFID 239   ::::	Qy 123 AAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK 180	Qy 64 TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY 122 ;	Db 57 RICVCVRKRPLNKQELAKKEIDVISIPSKCLLLVHEPKLKVDLTKYLENQAFCFDFAFDE 116
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Db Oy	g Q	Оу	ОУ	g . Q	дb
705 SDVQIRYVNENDTSKKNUNDIFFDAISCNNWYNNINTUNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	646 DISTKDENHN-DNKINNGVINIINNSNVNSINNSNMNSINNSNMNSNSIYKSNYNSNQSI 704 	586 VGSKLTMFSYDDQKNKDNTFFKSNINKMEDNTDKDILYESRNVSNMNGNVLLGLNKNTHH 645  :   :   :   :   :   :   :   :   :   :	526 FTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSSCDNIMNKKKNNLHLARHS 585	473 NNNNNDSSSMVNNMINHMINNNIN-NNINVNNNNNNNNNNNNNNHLPQPNYA 525	428 KIKKNKKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNNNNNNNNNN 472	318 -MNNINNNKDIIINRSGISNGNSQSVPCFENILDYDKLKFVEYINSFS 365

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RESULT 18
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; ORGANISM: Human
US-10-422-866-4
                                                                                                                                                                                                                                                                                                                                      US-10-422-866-2
                                                  FILE REFERENCE: 1054
CURRENT APPLICATION NUMBER: US/10/422,866
CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: US/09/722,129
PRIOR FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 132; Conserv
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                                                                                                                                                                                                                                                                               Sequence 2, Application US/10422866 Publication No. US20030170857A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: US/09/722,129
PRIOR FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: the
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APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. US20030170857A1el motor
TITLE OF INVENTION: their use
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LENGTH: 492
TYPE: PRT
ORGANISM: Human
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; OTHER INFORMATION: Xaa
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US-10-304-095-6
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US-10-304-095-6
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Best Local S
Matches 330
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Publication No. US20
GENERAL INFORMATION:
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APPLICANT: Metz, Anneke M.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT)
FILE REFERENCE: 47714-5009-US
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-06-14 NUMBER OF SEQ ID NOS: 49
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CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2184
TYPE: PRT
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                              FEATURE:
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KNYDFLSFSF----KTYKIINFMVYITKKCIPIKLLGSKHNF---KIFLKNVKKFLLF
                                                                NVINTKFGKIYRKFFPRKHILNKIHKIFKIIRLQIIKKYRIINIRMNRKFIKQKVYDTFF
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                              NGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFI 144
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Pred. No. 5.6e-29;
4; Mismatches 489;
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978 INSLNDYMSNTLLHFKEKYTYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNNVDNNN 1037 	918 SNNNNSSSSSSSNNNIYNNINDDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQNDDIIYT 977 	872NNMGNNNSPRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIK 917	828 DLNNKEQKDKNHGCDNNIIQNRNDFEKKKKTNFYNNNNIVIVN- 871	777 AYNSHNLFQPDNNKNTSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLI 827 	724 NIF-FDAISCDNNMYPNITNNNNNNNNNNNNNNNNIDVENYNNRDGTNNSMKLY 776 	681 NSINNSNMNSNSIYKSNYNSNQSISDVQIRYVNEMDTSNKNND 723	621 ILYESRNVSNMAGNVLLGLNKNTHHDISTKDENHNDNKINNGVINIINNSNVASINNSNM 680     -  -  -  -  -  -  -  -  -  -  -  -	568 CDNIMNKKKNNILHLARHSVGSKLTMFSYDDOKNKDNTFFKSNINKMEDNTPKD 620	508 NUNNNNSHNNHLPQDNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSS 567	448 NTINKKHNNINNINNINNINNINNINNINNINNINNINNINNINNI	409 PREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYND 447	390 KINDKIDK 408 ;	340CINEEDDTNTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNNKINRG 389	287 RDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKST 339	250VSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPF 286 :::::	191 ILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGSERGADT- 249	145 SFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILRVLTKEEL 190 
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Sequence 9, Application US/1015533
Publication No. US20030104003A1
GENERAL INFORMATION:
APPLICANT: Nguyen, Thanh V.
APPLICANT: James, Anthony A.
TITLE OF INVENTION: A No. US20030104003A1el Surface Protein of the Malaria Parasite
FILE REFERENCE: 48417/CAB/R2682
CURRENT APPLICATION NUMBER: US/10/155,533
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO
SEQ ID NO
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-155-533-9
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                                          395
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                                                                                                                                                                                                                                                                                                     237
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646 DISTKDENHNDNKINNGVINIINNSNVNSINNSNMNSINNSNMNSNSIYKSNYNSNQS1S 705
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                                                                                     KSNINKMED---
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                                          KNKANLGDDIEDMNDFFEKDQPVHVKILGINTKKNIFYLG-NIIKYNENIKLSKGEYSKG 453
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APPLICANT: Peter Deak
APPLICANT: David M Glover
APPLICANT: Carcl Midgley
TITLE OF INVENTION: Cell cycle progression pr
FILE REFERENCE: CCI-021CP
CURRENT APPLICATION NUMBER: US/10/161,051
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: GB 0007268.6
PRIOR APPLICATION NUMBER: GB 0007268.6
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 119
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US-10-161-051-119
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                                                                              Query Match
Best Local S
Matches 152
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                                                                                                                                                                               ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                    LENGTH: 464
TYPE: PRT
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                                                                              al Similarity
152; Conser
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    HTNIKVAVRVRPYNVRELEQKQRSIIKVMDRSALLFDPDEEDDEFFFQGAKQPYR-DITK
                                       NSKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYID-----EPRYKVDMTK 48
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                                                                          7.2%; Score 491; DB 12; ilarity 31.3%; Pred. No. 1.6e-26; Conservative 73; Mismatches 169;
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                                                                                                                                                                                                                                                                                                      ; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Homo s
US-10-146-473-82
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US-10-146-473-82
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APPLICANT: Gure, Ali
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd
TITLE OF INVENTION: Breast Cancer Antigens
FILE REFERENCE: L00461/70130(JRV)
CURRENT APPLICATION NUMBER: US/10/146,473
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US 60/291,150
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Scanlan, Matthew APPLICANT: Gout, Ivan APPLICANT: Stockert, Elisabe APPLICANT: Gure, Ali APPLICANT: Chen, Yao-Tseng APPLICANT: Old, Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local Similarity
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  117 -PGIFQYAAGDIFTFLNIYDKDNTKG----IFI---SFYEIYCGKLYDLLQKRKMVAAL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDINKNTSLG---KIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LREDNNG----VVVSGLCLTPIYSAEELLRMLMLGNSHRTQHPTDANAESSRSHAIFQVHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALE--NGKKEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMNKKLTMEF--DRVFDIDNSNQDLFEECTAPL-VDAVLNGYNCSVFVYGATGAGKTFTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIERH---EFIVDKVFDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RITERKTDTKRTVKLSMIDLAGSERAASTKGIGVRFK-EGASINKSLLALGNCINKLADG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INEEDDTNTERISILDSK-GSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNN 399
                                                                                         VDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TTLKQNVLKSKMPTEFYVKKIDEVVAENERLK---
                                                              TTQESVFA-TVAKSIVESCMSGYNGTIFAYGQTGSGKTFTMMGP---SESDNFSHNLRGV
                                                                                                                                          IKVFVRIRPPAE-RSGSADGE----QNLCLSVLSSTSLRLHSNP--EPKTFTFDHVADVD
                                                                                                                                                                                  IKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDDT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stockert, Elisabeth
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                       6.7%; Score 460.5; DB 15; Length 1388
18.5%; Pred. No. 9.6e-24;
ative 262; Mismatches 517; Indels 477;
<del>..</del>
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                                                                                                                                                                                                       YGLCGSHTSIDNMKNNEMKNNEMKDN------
                                                                                DIERDMLCEDLAHATEQLNMLTEASKKHSGLLQSAQEELTKKEALIQELQHKLN----QK 1110
                                                                                                                                                                TSVCEKTETIDTLK-QELKDINCKYNSALVDREESRVLIKKQEVDILDLKETLRLRILSE
                                                                                                                                                                                                                                                   EQQMAKVQKLEESLLATEKVISSLEKSRDSDKK------VVADLM--NQIQELR
                                                                                                                                                                                                                                                                                                                                                                              LFQPDNNKNTSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLNNKEQKDKNIHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNIFFDAISCDNIMYPNITNINNNNNNNNNNNNNIDVENYNNRDGTNNSMKLYAYNSHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHS-----ADKELSSVKLEYSSFKTNOEKEFNKLSERHMHVQLQLDNLRLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNSNVNSINNSNMNSINNSNMNSNSIYKSNYNSNQ-----SISDVQIRYVNEMDTSNKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKME-DNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NNSKQEYEEFKELTRKRQLELESELQSL--QKANLNLENLLEATKACKRQEVSQLNK 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNTSLGKIA-----FIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAM----D
KEEVEQKKNEYN-----FKMRQLEHVMDSAAEDPQSPKTPPHFQTHLAKLLETQEQEIED 1165
                                         KNNTNINSNIYQNDDIIYTINSLNDYMSN-----TLLHFKE------
                                                                                                                                                                                                                                                                                                                                   EKL-LESKACLQDSYDNLQEIMKFEIDQLSRNLQNFKKENETLKSDLNNLMELLEAEKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMQELFSSERIDWTKQQEELLSQLNVLEKQLQETQTKNDF-LKSEVHD------LRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKDILYESRNV--SNMNGNVLLGLN------KNTHHDISTKDENHNDNKINNGVINII 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVPPEMNEQAFEAISEELRTVQEQMSALQAKL----DEEEHK-NLKLQQHVDKLEHHST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEKAFSEISGMEKSDKNQQGFSPKAQKEPCLFANTEKLKAQLLQIQTEL------
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                                                                                                                         HIKSNNNNSSSSSSSNNNIYNNINDD----DTFQNDYCHNDNTFTIRR
                                                                                                                                                                                                                                                                                            ----IQNRNDFEKKKKTNFYNNNNIVIVNNNMGNNNSPRMK
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CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US/99/762,154
PRIOR APPLICATION NUMBER: ED 98202634.6
PRIOR APPLICATION NUMBER: EP 98202634.6
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 1269
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-342-224-62
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US-10-342-224-62
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Best Local Similarity
Matches 129; Conserv
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Publication No.
                                                                                                                                                                                                         1053
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APPLICANT: Nathalie Verbruggen
TITLE OF INVENTION: Genes Involved in Tolerance
FILE REFERENCE: CNN-012US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1355 YVV--RIKKENVRIAE-----ETEKIRAENVFIKEKKRSES 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 GIFQYAAGDIFTFLNIYDKDNTKGIF-ISFY--EIYCGKLYDLL----QKRKMVAALENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               946 FDMRASQDDIFEDT-KYLVQSAVDGY-NVCI---FAYGQTGSGKTFTI----YGHESNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNSKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKV
                                                                                                          DSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKN-KSTCINEEDD
                                                                                                                                                                                                     GLTPRATKELF---NILKRDSKRFSFSLKAYMVELYQDTLVDLLLPKSARRLKLEIKKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKGKIRVYCRIRPLNEKESSEREKOMLTTVDEFTV---EHAWKDD-----KRKOHIYDRV
TNTERI -----SILDSKGSEMNASSIE 368
                                                      NHKLIMLMSDSLGGNAKTLMFVNVSPAESNLDETYNSLLYASRVRTIVNDPSKHISSKEM 1231
                                                                                                                                                                          QSAARGKLSFVDLAGSERVKKSGSAGCOLK-EAQSINKSLSALGDVIGALSSGNQHIPYR
                                                                                                                                                                                                                                                                                                                         KKEVVVKDLKILRVLTKEBLILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNT
                                                                                                                                                                                                                                                                                           KGMVFVENVTTIPISTLEELRMILERGSERRHVSGTNMNEESSRSHLILSVVIESIDLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDDTVDNFTVYENTIKPLI---IDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.6%; Score 454.5; DB 1
33.3%; Pred. No. 2.3e-23;
vative 80; Mismatches 137
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                                                                                                                                                               RESULT 26
US-09-883-096-2
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                                       GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Cravven, Andrew
APPLICANT: Yu, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                       Sequence 2, Application US/09883096 Patent No. US20020110883A1
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Best Local
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TITLE OF INVENTION: NOVEL MOTOR PROTEINS /
FILE REFERENCE: 020552-0014410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
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APPLICANT: Craven, Andrew
APPLICANT: Yu, Ming
APPLICANT: Sakowicz, Roman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
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                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Similarity 32.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSTLQVVVRVRPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGTHDGPKKK 64
                                                                                                                                                                                                                                                                                    KNHIPFRDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNK 337
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                                                                                                                                                                                                                                                                                                                                                             --INKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAM---DSD 280
                                                                                                                                                                                                                                                                                                                                                                                                         PDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAIFQIFVKQQDRV 238
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Yu, Ming
Sakowicz, Roman
Patel, Umesh A.
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Pred. No. 5.9e-24;
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US-10-157-031-38
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                                                                ; TYPE: PRT
; ORGANISM: Homo
US-10-157-031-38
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/101 Publication No. US20030108890A1 GENERAL INFORMATION:
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                                                                                                                                                       SEQ ID NO 38
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS
FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR PILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                              APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening
FILE REFERENCE: 2760-103
                                                                                                                                                                                                                     FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baranova, A. V. APPLICANT: Yankovsky, N.
                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Amino acid sequence encoded by human kinesin motor OTHER INFORMATION: protein gene HsKip3a (Figure 1).
OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence of HsKip3a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
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  ,88°61,
  Score 446; DB 15;
Pred. No. 1.3e-22;
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Matches

284;

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                                                 NSPRMKYGLC----GS-----HTSIDNMKNNEM------KNNEMKDNEM
                                                                                                                                                                                  TSIRVRNLKLGISTFWSLEKFESKLAAMKELYESNGSNRGEDA----FCDPEDEWEPDI
                                                                                                                                                                                                                                                                            ---QILQQNRNNRDKTFTVQTTWSSMKLSMMIQEANAISSKLKTYYVFGRHDISDKSSSD
                                                                                                                                                                                                                                                                                                                                                                    EMETLATKQALEDHSIRHARILEALETEKQKIAKEV------------
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                                                                                            TDAPVSSLSRRRSRSLMKNRRISGCLHDI-----QVHPIKNLHSSHSSGLMDKSSTIYSN
                                                                                                                                                                                                                                                                                                                         NNNNIDVENYMNRDGTN-----NSMKL------YAYNSHNLFQPDNNK 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----IKALEAELREESQRKKMQEINNQKA----NHKIEELEKAKQHLEQEIYVNKKRL
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                                                                                                                                     NNKEQKDKN I HGCDNN I I QNRNDFEKKKKTNFYNNNN I VI VNNNMGNN
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US-09-883-096-4
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APPLICANT: Craven, Andrew
APPLICANT: Yu, Ming
APPLICANT: Sakowicz, Roman
APPLICANT: Bakowicz, Roman
APPLICANT: Davies, Katherine A.
TITLE OF INVENTION: NOVEL MOTOR PROTEINS AND ME
FILE REFERENCE: 020552-001410US
CURRENT APPLICATION NUMBER: US/09/883,096
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR APPLICATION NUMBER: US 09/594,655
PRIOR APPLICATION DATE: 2000-06-15
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LENGTH: 338
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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SOFTWARE: PatentIn Ver. 2.1
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170 GKKEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKD----
                                                                    117 --GREGDPGIMYLTTVELYRRLEARQQEKHFEVLİSYQEVYNEQIHDLLEPKGPLAIRED
                                                                                                             110 PYGQSDTPGIFQYAAGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALEN
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                                                                                                                                                          61 GKDLTFVFDRVFGEAATQQDVFQHTTHS-VLDSFLQGYNCSVFAYGATGAGKTHTML---
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                                                                                                                                                                                                                                                                                               2 NSKIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYI--DEPRYKVDMTKYIERHE----
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                                                                                                                                                                                                     ----FIVDKVFDDTVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQ 109
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RESULT 30
US-10-167-831-2
; Sequence 2, Ap;
; Publication No
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US-09-847-874A-1
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APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/847,874A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/467,946
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PERL Program
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TITLE OF INVENTION: KINESIN-LIKE MOTOR PROTEIN
FILE REFERENCE: PF-0593 US
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OTHER INFORMATION: 128
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TYPE: PRT
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Application US/10167831
No. US20030166209A1
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                                                                                                                                                                                                                                                           TGLD-SEKVSKISLVDLAGSER-ADSSGARGMGLKEGANINKSLTTLGKVISALADMQSK 291
                                                                                                                                                                                                                                                                                             KDINKNTSLGKIAFIDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRA---MDSD
                                                                                                                                                                                                                                                                                                                                                                      KEVVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNI------DL
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PGIFQYAAGDIFTFLNIYDKDNTK---GIFISFYEIYCGKLYDLL--QKRKMVAALENGK 171
                                                                                                             NAIINE--DPNARLIRELQEEVARLRELLMAQGLSASALEGL 390
                                                                                                                                               STCINEEDDTNTERISILDSK-----GSEMNASSIENV 370
                                                                                                                                                                                    KRKSDFIPYRDSVLTWLLKENLGGNSRTAMIAALSPADINYEETLSTLRYADRTKQIR-C
                                                                                                                                                                                                                      K---NHIPFRDSELTKVLRDIFVGKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNK 337
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APPLICANT: Shuman, Stewart
APPLICANT: Ho, C. Kiong
ITILE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
ITILE OF INVENTION: for Treatment of Parasitic Infections
FILE REFERENCE: D6388D
CURRENT APPLICATION NUMBER: US/10/167,831
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 09/752,165
PRIOR APPLICATION NUMBER: US 09/752,165
PRIOR EILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 2
LENGTH: 596
TYPE: PRT
ORGANISM: Plasmodium falciparum
FEATURE:
NAME / KEV. DEDTINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NNNIHIHNSGNNTNQTHSYDKNADDNKPTCNYSY------
                                      KSLQTI--NEVHVENKWKAFKRGTKIEVLLCSDDEEYEQNEDVQDINNEYYDQYKNEEDT
                                                                        YTYPTLSTNE-DIYNKEMEGKH-----IRLDDQDKYDDND-----NNNVDNNNKNNVDN 104:
                                                                                                               EKFKKYIHSVLPIVGDYMYRVVTKNEKHİKRKİ--KDQLİTNKEKINIFKNNVDIRRHNK
                                                                                                                                                 ----DYCHN-----DUTFTIRRKNNTNINSNIYONDDIIYTINSLNDYMSNTLLHFKEK
                                                                                                                                                                                                                      SHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSSSSSSSNNNIYNNINDDDTFQN--- 945
                                                                                                                                                                                                                                                             TKNNELYEVEIEIPSKTIFKAMSNLRNKKDSNYLH-----FICSNLVNNIR-----GIC-
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21.5%;
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Pred. No. 3.7e-19;
Pred. Mismatches 245;
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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-363-798-2
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US-10-363-798-2
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APPLICANT: YU., Chuan
APPLICANT: Hu, Landian
APPLICANT: Hu, Landian
TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOGENESIS IMPERFECTA
TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND CODED
TITLE OF INVENTION: PRODUCT THEREOF
FILE REFERENCE: 9548.780SWO
CURRENT APPLICATION NUMBER: US/10/363,798
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: CN 00125042.6
PRIOR APPLICATION NUMBER: CN 00125042.6
PRIOR APPLICATION NUMBER: CN 00125042.6
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.5%; Score 376.5; DB 12; Length 1253 Best Local Similarity 19.2%; Pred. No. 6.9e-18; Matches 159; Conservative 193; Mismatches 334; Indels 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kong, Xiangyin APPLICANT: Xiao, Shangxi
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    DSSDSSNSSDSSDSSDSSDSSDSSDSSDSS-----
                                     MKLYAYNSHNLFQPDNNKNTSNIQNINTNKNNQDGNVNYSMNFCHYNLNDKNYLIDLNNK
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    -NSSDSN---DSSNS
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US-10-304-095-8
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Best Local Similarity. Z1...
714; Conservative
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PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 794
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10304095
Publication No. US20030134275A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Long, David M.
APPLICANT: Metz, Anneke M.
APPLICANT: Love, Ruschelle A.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase
FILE REFERENCE: 47714-5009-US
CURRENT APPLICATION NUMBER: US/10/304,095
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Plasmodium falciparum
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                                       FKNLLLKKKIWGSNI-NSSKTKIFKIPLIYKNDLLIYNFQNKYQQKKKYKIKNKKKIQSV
                                                                                                                      YYAYLDKNEESQNLLYSEKQINNKYFLANGTCNYFNLNSLILRFIDDFLFITLNKKNIKI
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21.6%; Pred. No. 5.2e-18;
tive 152; Mismatches 312
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RESULT 33
US-10-087-464-47
; Sequence 47, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
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                                                                                                                                                                            SOFTWARE: Pa
                                    Matches 169;
                                                                     Query Match
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TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
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APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Goel, Vikas
                                                                                                                                                           LENGTH: 1191
                                                      Local Similarity
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                                  Conservative 137;
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                                                 5.5%; Score 373; DB 15; 21.0%; Pred. No. 1.1e-17;
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                                    Mismatches
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                                    371;
                                                                   Length 1191;
                                    Indels 128;
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; Sequence 107, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
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                                                 APPLICANT: Council of Scientific and Industrial Research TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTITITE OF INVENTION: USEFUL AS ANTI-INFECTIVES FILE REFERENCE: 063915 CURRENT APPLICATION NUMBER: US/09/820,843A CURRENT FILING DATE: 2001-03-30 NUMBER OF SEQ ID NOS: 118 SOFTWARE: Patentin version 3.0 SEQ ID NO 107
   LENGTH: 665
TYPE: PRT
ORGANISM: Plasmodium falciparum
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                                                                                 Sequence 12996, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith V APPLICANT: Wall, Daniel
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OTHER INFORMATION: hypothetical
NAME/KEY: misc feature
OTHER INFORMATION: gi|3845248
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-102-16
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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Best Local Similarity
Matches 237; Conserv
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                                                             YRDAEQSKKTAYDQAVAAAKAILNKQTGSNSDK--
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18.9%; Pred. No. 1.5e-14;
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RESULT 36
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                                                                                                                                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 1228
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
NAME/KEY: SITE
LOCATION: (75)
OTHER INFORMATION: X
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Craig Rosen, APPLICANT: Steve Ruber
                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                       ORGANISM: Homo FEATURE:
                                                                                                                             TYPE: PRT
                                                                                                                                                    ENGTH:
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NAME/KEY: SITE
LOCATION: (435).
; OTHER INFORMATION: Xaa
US-09-925-300-1228
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; ORGANISM: Homo US-10-171-311-196
                                                                NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 196, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-66-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
                                                                                                                                                                                                                    FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
                                                                                                                                                                                                                                                                     APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: OF CERVICAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schlegel, Robert APPLICANT: Chen, Yan
                                 TYPE: PRT
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                                                 LENGTH: 890
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Kamatkar, Shubhangi
Glatt, Karen
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Zhao, Xumei
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Pred. No. 1.:
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Query Match
Best Local Similarity
Matches 117; Conserv

Conservative

4.9%; Score 333.5; DB 1 25.7%; Pred. No. 4.7e-15; tive 64; Mismatches 128

DB 15;

Length

Indels

147;

Gaps

15;

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DUFFY, PATRICK E.
APPLICANT: OCKENHOUSE, CHRISTIAN F.
FILE OF INVENTION: SEQUESTRIN
FILE REFERENCE: 38644-175519
CURRENT APPLICATION NUMBER: US/09/351,794A
CURRENT FILING DATE: 1995-07-13
PRIOR APPLICATION NUMBER: 08/559,896
PRIOR FILING DATE: 1995-11-17
NUMBER: OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 652
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-09-351-794A-2
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US-09-351-794A-2
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Best Local S
Matches 176
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                                                                                                                                                                                                                                        y Match
4.9%; Score 333; DB 9; 1
Local Similarity 21.5%; Pred. No. 3.4e-15;
nes 176; Conservative 132; Mismatches 283;
158
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                                                                                                                                                                                                           335 KNKSTCINEEDDTNTERISILDSKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDK 394
                                                                                                                   60 MGKEEIETYFKGNIDKKSLDE-----FHKI-LLEELNKMDKDELYEM--YREEL---
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                       NNNNNNSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSS
                                                        NRIEQQKIRNMNKQQINKTYKDEINNMNSDQVDKIHREELEKIEKEKI-----NKMD
                                                                                      IERNNI-----LKNKSFDKPREGFTSTFGKYSSLNDIDKIKKNKKKGLINYKSTLYND
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KDEIDKIYREELDKMD---RDAIYSMYIEDIS---NKNIKDLI---KNEKETNKDKNKKK 208
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US-09-801-368-392
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TYPE: PRT
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1059 KWNVDNNWVDNDDDDDDDDFHNIKNFNNNEYLSYFQKWV 1095
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616 NNSVDIYNVEHIDEAEKKPNLDNPKKFDWTQVFKDKV
                                                                                                                                                                                                                                                                             945 NDYCHNDNTFTIRRKUNTNINSNIYQNDDI--IYTINSLNDYMSNTLLHFKEKYTYPTLS 1002
                                                                                                                                                                                                                                                                                                                                                                                       889 SHTSIDNMKNNEM----KUNEMKDNEMKDNHIKSNNNNSSSSSSSNNNIYNNINDDDTFQ
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                                                                                                               SVDDINNVDGI KNVDG---I KNVDGI KNVDGI NNVGDI NNAGDI NNAGDI NNV---
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US-09-801-368-392
US-09-801-368-392
IS Sequence 392, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Hecht, Peter
APPLICANT: Hecht, Peter
APPLICANT: Holtman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Madden, Kevin
APPLICANT: Mo. US20020128250A1man, Thea
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Salama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Silama, Sofie
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1099;10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 392
LENGTH: 1093
TYPE: PRT

Production

in Fungi

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; ORGANISM: Saccharomyces cerevisiae US-09-801-368-392
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Matches 232
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Local Similarity 18.7%; Pred. No. 1.8e-14;
hes 232; Conservative 184; Mismatches 381;
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                                                   SKILENSPILYRRRSQSIS----DEKEKAKDNEN---QVEKKKDPLNSVKTAMPSLESPSS
                                                                                                                                                      NDDDTFQNDYCHNDNTFTIRRKNNTNINSNIYQNDDIIYTINSLNDYMSNTLLHFKEKYT
                                                                                                                                                                                                                         --PRMKYGLCGSHTSIDNMKNNEMKNNEMKDNEMKDNHIKSNNNNSSSSSSSNNNIYNNI 937
                                                                                                                                                                                                                                                                                           DLNNKEQKDKNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIVIVNNMGNNNS-----
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                                                                                                                      TDSEVNESQYLHSN-----
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                                                                                   YPTLSTNEDI YNKEMEGKHIRLDDQDKYDDNDNNNVDNNNKNNVDNNVDN-----
                                                                                                                                                                                                                                                           -GASTDIL----NLDNESPASIMNKFNTPAGGSNSRNNNTKADRKLAR
                                                                                                                                                                                      --YQQQQQQQPQNNVKIPKIIKTQHPDKEDSTADVNIAK--
                                                                                                                    -QPNSTNMNT-----IMEDLSNINSFVTSSVIKDIKSTP
NNVDNNVDN-----NDKNNVDNNNVDNDDDDVDFHNIKN 1081
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TITLE OF INVENTION: Genes Involved in Tolerance to
FILE REFERENCE: CNN-012US
CURRENT APPLICATION NUMBER: US/10/342,224
CURRENT FILING DATE: .2003-01-13
PRIOR APPLICATION NUMBER: US/09/762,154
PRIOR FILING DATE: .2002-02-02
PRIOR FILING DATE: .2002-02-02
PRIOR APPLICATION NUMBER: EP 98202634.6
PRIOR APPLICATION NUMBER: EP 98202634.6
PRIOR FILING DATE: 1398-08-04
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 959
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US-10-342-224-40
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Publication No. US20030162294A1
GENERAL INFORMATION:
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Similarity 23.8%;
76; Conservative 11
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                                                                                                                                                                                                                                                                                         SLRDI---LGDSDQDGVTFVQVTVLEVYNEEIYDLLSTNSSNNLGIGWPKGASTKVRLEV
                                                                                                                                                                                                                                                                                                                                                              EQEGLEEFYKKFIEERIKGV-KVGNKCTIMMYGPTGAGKSHTM-----FGCGKEPGIVYR
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                     YGGDESASAVILGSRIAAMDEFIIKLQSEKKQKEKERNEAQKQLKKKEEEVAALRSLLTQ
                                                     ---DDTNT----ERISILD------SKGSEMNAS-----SIENVVIKSNHLLSN
                                                                                      RDSKLTMLLQDSFEDDKSKILMILCASPDPKEMHKTLCTLEYGAKAKCIVRGSHTPNKDK
                                                                                                                        RDSELTKVLRDIFV-GKSKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEE-
                                                                                                                                                      --GRLMLVDMAGSE----NIDQAGQTGFEAKMQTAKINQGNIALKRVVESIANGDSHVPF
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3%; Pred. No. 1.9e-14;
118; Mismatches 305;
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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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              4100100
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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAG41923
AAG41922
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ABB58104
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Arabidopsis thalia
Arabidopsis thalia
Drosophila melanog
Plasmodium falcipa
Human KinI-3 DNA f
                                                                                                                                                                                                                                                                                                                                                           Description
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## ALIGNMENTS

AAR11019;

AAR11019 standard; Protein; 590

B

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RESULT 1
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                                                                                                                                                                                                                             Apo-lipoprotein \mathbf{E}; cell differentiation; hypercholestrolaemia; androgen; diagnosis.
                                                                                                                                                                                                                                                                                            25-MAR-2003
17-MAY-1991
                                                                      Region
                                                                                                                                                                                                                                                                   Apo-lipoprotein E induced cell differentiation copying polypeptide
                                                                                                                                                                                                                                                                                          (updated)
(first entry)
  21..130
21..130
/label= repeated_segment
/note= "present at least twice"
                                                                      /label=
56..76
                                                                                             /label= leader_segment
/note= "may be replaced by NH2"
21..40
/label= first_spacing_segment
/note= "may be omitted"
41..55
                                                                                                                                                                               Location/Qualifiers
                                                           label=
                                                        second_spacing_segment
                                                                                   p(141-155)
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kinesin moto

492

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434

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Matches
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26-FEB-1990;
18-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A polypeptide capable of inhibiting lymphocyte proliferation and/or ovarian androgen secretion comprises a plurality of segments, as indicated in the features. The segment may be repeated 2-10 times. In this example the segment is repeated 10 times. The N-terminal may comprise NH2 or a leader segment of 1-20 amino acids, the C-terminal comprises COOH or a tail segment of 1-20 amino acids. Between each segment is a first and second spacing segment of 1-20 amino acids. p(141-155) is a peptide obtained from apo E. See also AARILI107 and AARILI109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide(s) copying apo-lipoprotein E induced cell differentiation - useful for treating hypercholestrolaemia, inhibiting ovarian androgen secretion and for prodn. of diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 98; 123pp; English.
LNNKEQKDKNIHGCDNNIIQNRNDFEKKKKTNFYNNNNIVIVNNNMGNNNSPRMKYGLCG
                                                                                                                                            NNNN
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llarity 32.4%;
Conservative (
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90US-0485158.
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Pred. No. 4.4e-45;
9; Mismatches 215
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                                                                                       Arabidopsis thaliana
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                    Similarity
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Pred. No. 3e-36;
3; Mismatches 183;
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                                                                                 23-MAR-2001; 2001WO-US09231.
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                                                                                                                           WO200171042-A2
                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                     Drosophila
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                                                                                                                                                                                                   melanogaster polypeptide
          Adams M,
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                                                 2000US-191637P
2000US-0614150
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        PWD,
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          Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and in elucidating cell signalling and insections in higher eukaryoter the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
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  Plasmodium
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                                                                                   standard;
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CC The present invention describes proteins and their tragments (1) curve.

CC by chromosome 2 of the human malarial parasite, plasmodium falciparum.

CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2)

CC vaccines against p. falciparum infection comprising (I) or (II).

CC (I) and (II) are useful for the development of vaccines against

CC p. falciparum infection. (I) and polyclonal antisera or a monoclonal

CC antibody raised to immunogens comprising the sequences of (I), are

CC useful in the detection of infection with p. falciparum. Furthermore,

CC (I) (especially when they are rifins or secreted or membrane proteins)

CC can aid the identification of drugs to treat or grevent p. falciparum

CC p. falciparum. Sequencing of the plasmodium chromosome 2 and the

CC subsequent identification of proteins encoded by it will help to expand

CC our understanding of parasite biology, a process hampered by the

CC complexity of the parasite biology, a process hampered by the

CC vaccine and drug development. Parasite resistance to drugs and mosquito

CC resistance to insecticides have led to a resurgence of malaria in many

CC parts of the world, and there is a pressing need for vaccines and new

CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
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antimalarial; malaria; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and protein sequences given in the present invention, specifically mentioned within the specification.
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                                                                                                                                                      The invention relates to a human kinesin motor protein (KinI-3), with microtubule depolymerisation activity, and the polymucleotide encoding it. The novel KinI-3 motor protein can be used to prepare compositions for the diagnosis, prevention or treatment of cellular proliferation disorders, cancers, hyperplasias, restenosis, vascular malfunctions, abnormal wound healing, cardiac hypertrophy, inflammatory and immune disorders (such as rheumatoid arthritis, gout, psoriasis and diabetic retinopathy) neurological disorders and disorders of vesicular transport. This sequence represents a human KinI-3 polypeptide fragment with
                                                                                                                                        retinopathy) neurological combines sequence represents a flanking vector sequences.
                                                                                                                                                                                                                                                                                                                              An novel isolated microtubule motor protein, KinI-3 used for preparing compositions for the diagnosis, prevention or treatment of diseases such as cancers, hyperplasias or restenosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; kinesin motor protein; KinI-3; microtubule; hyperplasia; depolymerisation; cellular proliferation disorder; cancer; restenosis; vascular malfunction; abnormal wound healing; cardiac hypertrophy; gout; inflammatory disorder; immune disorder; rheumatoid arthritis; psoriasis; diabetic retinopathy; neurological disorder; immunostimulant; vasotropic; vesicular transport disorder; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 68pp; English.
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                                                                                                                        The invention relates to a human kinesin motor protein (KinI-3), with microtubule depolymerisation activity, and the polymerisate encoding it. The novel KinI-3 motor protein can be used to prepare compositions for the diagnosis, prevention or treatment of cellular proliferation disorders, cancers, hyperplasias, restenosis, vascular malfunctions, abnormal wound healing, cardiac hypertrophy, inflammatory and immune disorders (such as rheumatoid arthritis, gout, psoriasis and diabetic retinopathy) neurological disorders and disorders restricted and disorders and disorders restricted arthritis.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An novel isolated microtubule motor protein, KinI-3 used for preparing compositions for the diagnosis, prevention or treatment of diseases such as cancers, hyperplasias or restenosis -
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 68pp; English.
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                                                                                                    sequence represents a human KinI-3
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; kinesin motor protein; KinI-3; microtubule; hyperplasia; depolymerisation; cellular proliferation disorder; cancer; restenosis; vascular malfunction; abnormal wound healing; cardiac hypertrophy; gout; inflammatory disorder; immune disorder; rheumatoid arthritis; psoriasis; diabetic retinopathy; neurological disorder; immunostimulant; vasotropic, vesicular transport disorder; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Domain
                       An novel isolated microtubule motor protein, KinI-3 used for preparing compositions for the diagnosis, prevention or treatment of diseases such as cancers, hyperplasias or restenosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic.
                                                                                                                            N-PSDB;
                                                                                                                                                                                                     Beraud
                                                                                                                                                                                                                                                                                                        29-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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)B; ABK47997.
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                                                                                                                                                                                                        Freedman
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47.5%; Pred. No. 1.3e-35;
tive 58; Mismatches 116;
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RESULT 10
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Best Local S
Matches 164
                                                                                                                                                                                                             vascular malfunction; abnormal wound healing; cardiac hypertrophy; gout; inflammatory disorder; immune disorder; etinopathy; neurological disorder; immunostimulant; vasotropic; vesicular transport disorder; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a human kinesin motor protein (KinI-3), with microtubule depolymerisation activity, and the polymucleotide encoding it. The novel KinI-3 motor protein be used to prepare compositions for the diagnosis, prevention or treatment of cellular proliferation disorders, cancers, hyperplasias, restenosis, vascular malfunctions, abnormal wound healing, cardiac hypertrophy, inflammatory and immune disorders (such as rheumatoid arthritis, gout, psoriasis and diabetic retinopathy) neurological disorders and disorders of vesicular transport. This sequence represents the human KinI-3 polypeptide.
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                              29-SEP-2000; 2000US-0675227
                                                          28-SEP-2001; 2001WO-US30750
                                                                                                                        WO200226929-A2
                                                                                                                                                    Synthetic.
                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                 cytostatic.
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(CYTO-) CYTOKINETICS INC
                                                                                                                                                                                                                                                                             depolymerisation;
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                                                                                                                                                                                                                                                                                                                        KinI-3
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                                                                                                                                                                                                                                                                       motor protein; KinI-3; microtubule; hyperplasia;
on; cellular proliferation disorder; cancer; restenosis;
                                                                                                                                                                                                                                                                                                                    fragment with flanking vector sequences
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Pred. No. 5.3e-35;
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RESULT 11
AAUT7183
ID AAUT7
XX AAUT7
XX AUT7
XX O2-JU
XX Human
XX Human
KW depoll
KW vascu
KW diable
KW vesic
KW vesic
XX Cytos
XX Homo

Human KinI-3

DNA fragment with

flanking vector sequences

(first

entry)

AAU77183

standard;

Protein;

373

Human; kinesin motor protein; KinI-3; microtubule; hyperplasia; depolymerisation; cellular proliferation disorder; cancer; restenosis; vascular malfunction; abnormal wound healing; cardiac hypertrophy; gout; inflammatory disorder; immune disorder; rheumatoid arthritis; psoriasis; diabetic retinopathy; neurological disorder; immunostimulant; vasotropic; vesicular transport disorder; immunosuppressive; antiinflammatory;

Homo sapiens

cytostatic.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An novel isolated microtubule motor protein, I compositions for the diagnosis, prevention or such as cancers, hyperplasias or restenosis -
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                                                                                                                                                                                                                                                                                                                                                4 KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector
                                                                                                                                                                                                                                                     ACTNQDVYMKTTHPLIQHIF-NGGNATCFAYGQTGAGKTYTMIGTH-----ENPGLYALA
                                                                                                                                                                                                                                                                                    TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA
KTCMIANISPSHVATEHTLNTLRYADRVK
                KSIMIANISPTISCCEQTLNTLRYSSRVK
                                                           ERAADARDSDROTKMEGAEINQSLLALKECIRALDQEHTHTPFRQSKLTQVLKDSFIGNA
                                                                                          ERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKS
                                                                                                                          VDSVELLLEVILKGSKERSTGATGVNADSSRSHAVIQIQIKDSAKRT-FGRISFIDLAGS
                                                                                                                                                       VLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDLAGS
                                                                                                                                                                                       AKDIFRQLEVSQPRKHLFVWISFYEIYCGQLYDLLNRKKRLFAREDSKHMVQIVGLQELQ
                                                                                                                                                                                                                      AGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKWVAALENGKKEVVVKDLKILR
                                                                                                                                                                                                                                                                                                                    KIRVCVRKRPLGMREVRRGEINIITVEDKETLLVHEKKEAVDLTQYILQHVFYFDEVFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guo
                                                                                                                                                                                                                                                                                                                                                                                                                                               343 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68pp;
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                                                                                                                                                                                                                                                                                                                                                                                                11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                 58;
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                                                                                                                                                                                                                                                                                                                                                                                                Score 758.5; DB 2
Pred. No. 4.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                            332
                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davies KA;
                                                                                                                                                                                                                                                                                                                                                                                 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KinI-3 used for preparing 
c treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                 7;
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RESULT 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a human kinesin motor protein (KinI-3), with microcubule depolymerisation activity, and the polymucleotide encoding it. The novel KinI-3 motor protein can be used to prepare compositions for the diagnosis, prevention or treatment of cellular proliferation disorders, cancers, hyperplasias, restenosis, vascular malfunctions, abnormal wound healing, cardiac hypertrophy, inflammatory and immune disorders (such as rheumatoid arthritis, gout, psoriasis and diabetic retinopathy) neurological disorders and disorders of vesicular transport. This sequence represents a human KinI-3 polypeptide fragment with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An novel isolated microtubule motor protein, K compositions for the diagnosis, prevention or such as cancers, hyperplasias or restenosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-352124/38.
N-PSDB; ABK47998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                 02-FEB-2000
                                          AAY49949;
                                                                    AAY49949
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                                                                                                                                                                                                                                                                                                                                                                                     TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGSQPYGQSDTPGIFQYA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector
                                                                  standard;
                                                                                                                                       KSIMIANISPTISCCEQTLNTLRYSSRVK
                                                                                                                                                                                                             ERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIFVGKS
                                                                                                                                                                                                                                                  VDSVELLLEVILKGSKERSTGATGVNADSSRSHAVIQIQIKDSAKRT-FGRISFIDLAGS
                                                                                                                                                                                                                                                                                                                                  AGDIFTFLNIYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLKILR
                                                                                                                                                                                                                                                                                                                                                           ACTNODVYMKTTHPLIQHIF-NGGNATCFAYGQTGAGKTYTMIGTH-----ENPGLYALA
                                                                                                                                                                                                                                                                                                                                                                                                                   KIRVCVRKRPLGMREVRRGEINIITVEDKETLLVHEKKEAVDLTQYILQHVFYFDEVFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                           KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
                                                                                                                                                                                            ERAADARDSDROTKMEGAEINQSLLALKECIRALDQEHTHTPFRQSKLTQVLKDSFIGNA
                                                                                                                                                                                                                                                                                                      AKDIFRQLEVSQPRKHLFVWISFYEIYCGQLYDLLNRRKRLFAREDSKHMVQIVGLQELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 3; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
               (first
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                                                                    Protein;
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48.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 758.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                    B
                                                                                                                                        363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KinI-3 used
r treatment o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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DSGGSH---ASIEGLOLODDFLLKDEELSTHN--SFQDALNRVGELEDKAVDELRE DSKGSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPRE 411 DSFIGENSRTCMIAMLSPGFNSCEYTLNTLRYADRVKELSPQNA-----ETNDDNLQME DIFVGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISIL LVDLAGNERGVDTASADRITRMKGAEINRSLLALKECIRALGQNKSHTPFRESKLTQILR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for identifying a modulator of microtubule (MT) depolymerisation by contacting a polymerised MT with an MT severing or depolymerisation by contacting a polymerised MT with an MT severing or depolymerising protein and a candidate agent in the presence of ATP or GTP, and detecting formation of tubulin monomers, dimmers or oligomers. The method is useful to detect agents that regulate the cytoskeleton and the cell cycle. Such agents have potential for use as anti-mitotic agents. The present sequence represents the xenopus laevis kinesin central motor 1 (XKCM1), which regulates microtubule dynamics during mitotic spindle assembly. XKCM1 localises to centromers and appears to regulate the polymerisation dynamics of microtubules, and so is suitable for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microtubule severing protein; microtubule depolymerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying agents that modulate microtubule depolymerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                               KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD 63
                                                                                                                                                                                                         AAGDIFTFLNIYDKDNTK----GIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKD
                                                                                                                                                                                                                                                                                   TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY
                                                                                                                                                                                                                                                                                                                                                   RICVCVRKRPLNKQELSKKEIDIISVPSKNIVLVHEPKLKVDLTKYLENQAFRFDFSFDE
LLEKQVISADD-VFKMIBIGSACRTSGQTFANTSSSRSHACLQIILR---RGSKLHGKFS
                                                                                                       LKILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSL-GKIA
                                                                                                                                                          TATNEVVYRFTARPLVQSIFEGG-KATCFAYGQTGSGKTHTMGGDFSGKSQNVSKGVYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hartman JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 66; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%;
42.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
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Pred. No. 9.6e-35;
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Best Local S
Matches 174
                                                                                                                                                                                                                                                                The invention relates to human MCAK (mitotic centromere-associated kinesin) protein, and its fragments that comprise a motor domain and directly or indirectly produce ADP or phosphate. The MCAK enzyme and its fragments are used in methods to identify compounds that modulate their activity. Modulators of MCAK are useful as therapeutic agents for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders, inflammation, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease. The present sequence is a human MCAK
                                                                                                                                                                                                                                                                                                                                                                                                                                            New human MCAK (mitotic centromere-associated kinesin) protein useful in identifying agents for use in the treatment of cellular proliferation disorders -
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; MCAK; mitotic centromere-associated kinesin; motor domain; cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 12; 44pp; English.
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18-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2000; 2000US-0594669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CYTO-) CYTOKINETICS INC
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                                                                                                                              4 KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
                                                                                                                                                                                     Similarity
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              AAGDIFTFLN--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMYVAALENGKKEVVVKDLK
                                                                                 TVDNFTVYENTIKELIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QFYGQSDTFGIFQY
                                                                                                            RICVCVRKRPLNKQELAKKEIDVISIPSKCLLLVHEPKLKVDLTKYLENQAFCFDFAFDE
ASRDVFLLKNOPCYRKLGLE-VYVTFFEIYNGKLFDLLNKKAKLRVLEDGKQQVQVVGLQ
                                                      TASNEVVYRFTARPLVQTIFEGG-KATCFÄYGQTGSGKTHTMGGDLSGKAQNASKGIYAM
                                                                                                                                                                                                                             405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakowicz R;
                                                                                                                                                                       Conservative
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99US-0314464.
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42.1%;
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                                                                                                                                                                    Score 752.5; DB 23;
Pred. No. 1.1e-34;
5; Mismatches 143;
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RESULT 14
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                                                   The invention relates to human MCAK (mitotic centromere-associated kinesin) protein, and its fragments that comprise a motor domain and directly or indirectly produce ADP or phosphate. The MCAK enzyme and its fragments are used in methods to identify compounds that modulat their activity. Modulators of MCAK are useful as therapeutic agents for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders, inflammation, autoimmune disease, arthritis, graft rejection,
                                                                                                                                                                                                              New human MCAK (mitotic centromere-associated kinesin) in identifying agents for use in the treatment of celluproliferation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease.
                                                                                                                                                                                   Claim 1; Fig 10; 44pp; English
                                                                                                                                                                                                                                                                                                                   Beraud
                                                                                                                                                                                                                                                                                                                                                                           20-APR-1999;
18-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human mitotic centromere-associated kinesin protein fragment #5.
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                                          inflammatory
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                                                                                                                                                                                                                                                                                     2002-089075/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFID
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                                                                                                                                                                                                                                                                           AAD24084.
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                                          bowel
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99US-0314464.
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                                          disease.
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                                        The present sequence
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Sequence

434 AA;

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RESULT 15
AAE14502
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Best Local S
Matches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; autoimmune diarthritis; graft rejection; inflammatory bowel disease.
New human MCAK (mitotic centromere-associated kinesin) protein identifying agents for use in the treatment of cellular
                                                                                                                                                                                              20-APR-1999;
18-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; MCAK; mitotic centromere-associated kinesin; motor domain;
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                                                             N-PSDB;
                                                                                                                     Beraud
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                                                             AAD24083.
                                                                                                                                                           CYTOKINETICS
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ilarity 42.1%;
Conservative 7
                                                                                                                   Sakowicz
                                                                                                                                                                                                                                                      2000US-0594669
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99US-0314464
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Pred. No. 1.2e-34;
5; Mismatches 143;
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                         15-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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417 TEEMEACS--NGALIPGNLSKEEEELSSOMSSFNEAMTQIRELEEKAMEELKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                              VGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSK 358
                                                                                                                                                                     LAGNERGADTSSADRQTRMEGAEINKSLLALKECIRALGQNKAHTPFRESKLTQVLRDSF
                                                                                                                                                                                               LAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIF
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                                                                                   IGENSRTCMIATISPGISSCEYTLNTLRYADRVKELSPHSGPSGEQ------LIQME
                                                                                                                                                                                                                                                                                                                                                                                                                            TASNEVVYRFTARPLVQTIFEGG-KATCFAYGQTGSGKTHTMGGDLSGKAQNASKGIYAM 189
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Pred. No. 1.3e-34;
5; Mismatches 143
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AAE14505 standard; Protein; 723 B

09-APR-2002 (first entry)

Human mitotic centromere-associated kinesin protein fragment

Homo cardiac hypertrophy; US6331424-B1 arthritis; graft cellular Human; MCAK; sapiens proliferation mitotic centromere-associated kinesin; motor domain; rejection; immune disorder; disorder; cancer; hyperplasia; autoimmune restenosis; disease;

2000US-0594669

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RESULT 17
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AC AAE14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 14; 44pp; English.
                       Human mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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  Human; MCAK; mitotic
                                             09-APR-2002
                                                                                         AAE14506 standard;
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18-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD
                                                                                                                                                                    GSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPRE
                                                                                                                                                                                                        VGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSK
                                                                                                                                                                                                                                                      LAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIF
                                                                                                                                                                                                                                                                                                ILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFID
                                                                                                                                                                                                                                                                                                                                                 AAGDIFTFLN--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK
                                                                                                                                                                                                                                                                                                                                                                                                TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY 122
                                                                                                                                               TEEMEACS -- NGALI PGNLSKEEEELSSQMSSFNEAMTQIRELEEKAMEELKE
                                                                                                                                                                                          IGENSRTCMIATISPGISSCEYTLNTLRYADRVKELSPHSGPSGEQ------LIQME
                                                                                                                                                                                                                                       LAGNERGADTSSADROTRMEGAEINKSLLALKECIRALGONKAHTPFRESKLTOVLRDSF
                                                                                                                                                                                                                                                                                   EHLVNSADD-VIKMIDMGSACRTSGOTFANSNSSRSHACFQIILR--AKGRMHGKFSLVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCAK (mitotic centromere-associated kinesin) protein useful fying agents for use in the treatment of cellular
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                                             (first entry
                       centromere-associated
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99US-0314464.
                                                                                         Protein;
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centromere-associated kinesin; motor domain;
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Pred. No. 2.1e-34;
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                     kinesin protein
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cellular proliferation disorder; cancer; hyperplasia; restenosis; cardiac hypertrophy; immune disorder; inflammation; autoimmune disease; arthritis; graft rejection; inflammatory bowel disease.

Homo sapiens.

US6331424-B1.
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New human MCAK (mitotic centromere-associated kinesin) protein useful in identifying agents for use in the treatment of cellular proliferation disorders -  $\,$ 

Disclosure; Fig 16; 44pp; English.

The invention relates to human MCAK (mitotic centromere-associated kinesin) protein, and its fragments that comprise a motor domain and directly or indirectly produce ADP or phosphate. The MCAK enzyme and its fragments are used in methods to identify compounds that modulate their activity. Modulators of MCAK are useful as therapeutic agents for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders, inflammation, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease. The present sequence is human MCAK protein. Sequence 725 AA;

Query Match 11.0%; Score 750.5; DB 23; Length 725;
Best Local Similarity 41.9%; Pred. No. 2.7e-34;
Matches 173; Conservative 76; Mismatches 143; Indels 21; Gaps 10;

4 KIKVVVPKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD 63

318 604 436 300 493 258 RICVCVRKRPLNKQBLAKKEIDVISIPSKCLLLVHEPKLKVDLTKYLENQAFCFDFAFDE 64 4 KIKVVVRKRPLSELEKKKKDSDIITVKNNCTLYIDEPRYKVDMTKYIERHEFIVDKVFDD TVDNFTVYENTIKPLIIDLYENGCVCSCFAYGQTGSGKTYTMLGS-QPYGQSDTPGIFQY TEEMEACS -- NGALIPGNLSKEEEELSSQMSSFNEAMTQIRELEEKAMEELKE GSEMNASSIENVVIKSNHLLSNNNNNKINRGKINDKIERNNILKNKSFDKPRE VGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCINEEDDTNTERISILDSK LAGNERGADTSSADROTRMEGAEINKSLLALKECIRALGONKAHTPFRESKLTOVLRDSF LAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRDIF EHLVNSADD. VIKMLDMGSACRTSGQTFANSNSSRSHACFQIILR -- AKGRMHGKFSLVD ILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFID ASRDVFLLKNQPCYRKLGLE-VYVTFPEIYNGKLFDLLNKKAKLRVLEDGKQQVQVVGLQ AAGDIFTFLN--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK TASNEVVYRFTARPLVQTIFEGG-KATCFAYGQTGSGKTHTMGGDLSGKAQNASKGIYAM IGENSRTCMIATISPGISSCEYTLNTLRYADRVKELSPHSGPSGEQ------LIQME 358 435 180 122 552 299 492 239 317 63

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RESULT 18
AAB18301
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                                                                                                                                                                                                                                                                                                           infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the Subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB181144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not represented.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum
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The invention relates to human MCAK (mitotic centromere-associated kinesin) protein, and its fragments that comprise a motor domain and directly or indirectly produce ADP or phosphate. The MCAK enzyme and its fragments are used in methods to identify compounds that modulate their activity. Modulators of MCAK are useful as therapeutic agents
                                                                                                                                                                                                                     New human MCAK (mitotic centromere-associated kinesin) protein useful in identifying agents for use in the treatment of cellular proliferation disorders -
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                                                                                 20-APR-1999;
18-MAY-1999;
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                                                                              Human; MCAK; mitotic centromere-associated kinesin; motor doma: cellular proliferation disorder; cancer; hyperplasia; restenosicardiac hypertrophy; immune disorder; inflammation; autoimmune
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     Homo sapiens
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identifying agents for use in the treatment of cellular
oliferation disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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ilarity 38.6%;
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Pred. No. 5.5e-34;
6; Mismatches 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2000;
09-JUL-2000;
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29-NOV-2000;
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DB; AAI58414.
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R, Drmanac R
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous

such as peripheral nervous injuries, peripheral

and

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                                                                                  Query Match
Best Local :
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                                                                                                                                                                         atherosclerosis, diseases of the digestive system, atopic dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout, Grave's disease, lupus crythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjorgren's syndrome, autoimmune thyroiditis, complications of cancer, extracorporeal circulation, viral, bacterial, fungal, parasitic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KINRELP shares 97% identity with murine kinesin-related protein KIP2. The invention provides expension vectors, host cells, agonists, antibodies and antagonists, as well as methods for treating disorders associated with expression of KINRELP. KINRELP and its agonists are used to stimulate cell proliferation, and to treat a disorder associated with increased apoptosis. Antagonists treat a disorder associated with increased apoptosis. Antagonists used to treat cancer and inflammation (claimed). Particularly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of human kinesin-related protein (KINRELP), as deduced from a consensus cDNA sequence (see AAX06945).
KINRELP shares 97% identity with murine kinesin-related protein
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 49-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New kinesin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-080955/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-1997;
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                                                                                Local
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                                 4
                                                                                Similarity
RICVCVRKRPLNKKETOMKDLDVITIPSKDVVMVHEPKOKVDLTRYLENOTFRFDYAFDD
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                                                                                                                                                                helminthic infections and trauma.
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                                                                              10.7%;
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                                                                63;
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                                                                              Score 732.5;
Pred. No. 2.
                                                                Mismatches
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                                                                                                 679;
                                                              25;
                                                              Gaps
                               63
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Novel nucleic acids and such as central nervous

polypeptides, useful system injuries -

for

treating disorders

Example 4; SEQ ID NO 2402; 10078pp; English

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09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
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19-OCT-2000;
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                                                                                                                                                                                Liu C,
Wang Z,
Zhou P,
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2000US-0598042.
2000US-0620312.
2000US-0653450.
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                                                                                                                                                            peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; Haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assays for receptor activity, arthritis and C.N.S disorders.
   WO200153312-A1
                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                      Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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Pred. No. 2.6e-33;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
13-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                            specification.
                                                                                                                                                                                                                                                                                                                                                                       C.N.S disorders.
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DB; AAI60199.
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Zhou
                                                                                                                                                                                                                                                                                                 Similarity
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IFVGK-SKSIMIANISPTISCCEQTLNTLRYSSRVKNFKNKSTCI-
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                                      IDLAGNERGADTSSADRQTRLEGAEINKSLLALKECIRALGRNKPHTPFRASKLTQVLRD
                                                    IDLAGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKNHIPFRDSELTKVLRD
                                                                                                       LKILRVLTKEELILKMID-GVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAF
                                                                                                                                      AARDVFLMLK---KPNYKKLELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVG
                                                                                                                                                  AAGDIFTFLNIYDKDNTK----GIFISFYEIYCGKLYDLLQKKKMVAALENGKKEVVVKD
                                                                                     LQEREVKCVED-VLKLIDIGNSCRTSGOTSANAHSSRSHAVFQIILR--RKGKLHGKFSL
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2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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ilarity 45.5%;
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Wehrman T,
Goodrich
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25-APR-2000; 2000US-0552317.

09-UUL-2000; 2000US-0598042.

19-UUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-CCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinjoinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                     (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                       Proteins encoded by chromosome Plasmodium falciparum, useful a diagnosis of P.falciparum infec
                                               Disclosure; Page 133-137;
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protozoacide; infection; insecticide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by chromosome 2 of the human malarial parasite, Plasmodium falciparum Also described are: (1) nucleotide sequences (II) encoding (I); and (vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, useful in the detection of infection with P. falciparum.
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                                                                    NKNI VNMLNLKNMKSINDLSVLINKNKPIHHVINGTEVQQKRSLS-NVQKLKTLNTFPNA
                                                                                                              KKNLRDNIKLKNRSSCDN---IMNKKKNNLHLARHSVGSKLTMFSYDPQKNKD-NTFFK-
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4; Mismatches 524;
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    Plasmodium falciparum; antimalaria; malaria;
    11-MAY-2000
                                                 WO200025728-A2
                                                                                              Plasmodium falciparum
                                                                                                                                                                                                          Plasmodium falciparum chromosome
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                                                                                                                                                                                                                                                                                                    AAB18311;
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protozoacide;
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DTFQN-DYCHN-DNTFTIRRKNNTNINSNIYQNDDI--IYTINSLNDYMSNTLLHFKEKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIKNNWNDMWYKMNNNMKDIMHIKDATNI--NKINN-----KLVNLNTNNCISYNSC 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSSNNGDIIL-LN------KKLVQDNIKNS------MDHNNIH 1286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVDNNVD-----NNNVDNNVDNNDKNNVDNNVDNDDDDDVDFHNIKNFNNNEYLSYFQK 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPTLSTNEDIYNKEMEGKHIRLDDQDKYDDNDNNNVDNNNKN----------
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                                                                                                  related
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infection;
                                 human malaria parasite; vaccine;
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   insecticide
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Matches 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Also described are: (1) nucleotide sequences (II) encoding (1); and () vaccines against P. falciparum infection comprising (I) or (II) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins encoded by chromosome 2 of the human Plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specifically mentioned within the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e present invention describes proteins and their fragments (I) encoded chromosome 2 of the human malarial parasite, plasmodium falciparum.
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CARUCCI D.
GARDNER M.
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SNVNSINNSNMNSINNSNMNSNSIYKSN----YNSNQSISDVQIRYVNEM-DTSNKNNDN
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                                  KNVQKT---EQNNLNHTYLNNNIINNI
                                                                DNTPKDILYESRNVSN--MNGNVLLGLNKNTHHDISTKDENHNDNK---INNGVINIINN
                                                                                                      NNKUNI NNNNNNNC - -
                                                                                                                                    NLRDNIKLKNRSSCDNIMNKKKNNLHLARHSVGSKLTMFSYDPQKNKDNTFFKSNINKME
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ilarity 26.6%;
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Pred. No. 3.6e-31;
1; Mismatches 300;
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                                WPI; 2001-656860/75.
N-PSDB; ABL03836.
                                                                                                                         23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                pharmaceutical.
                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 5991
                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                      ABB59733;
                                                                       Venter JC,
                                                                                                                                                              23-MAR-2001; 2001WO-US09231
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2000US-0614150
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New isolated nucleic acid genes from Drosophila and

detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell

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RESULT 31
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ID AAO22
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The inventi useful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

(ABB57737-ABB72072).
                                                                                                                                  Wooden leg; WOL; vascula wood production; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 5991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interactions
29-NOV-2000; 2000US-253739P
                                                                                                                                                                            Wooden leg
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                          29-NOV-2001; 2001WO-US45053
                                                                                WO200244337-A2
                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                        28-OCT-2002
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                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                             ----LGSTSMSDIVCQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQNPVQNTAEVLDLLELGNSVRTSGHTSANSKSSRSHAVFQIVLRSAAGEKLHGKFSLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILRVLTKEELILKMIDGVLLRKIGVNSONDESSRSHAILNIDLKDINKNTSLGKIAFID
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                                                                                                                                                                                                                                                                                                                                                        KGSEMNASSIENVVIKSN 375
                                                                                                                                                                                                                                                                                                                                                                                   IGGKKVKTCMIAMISPCLHSVEHTLNTLRYADRVKELSVESIPSKRMPDAN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 AA;
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                                                                                                                                                                                                       (first
                                                                                                                                   vasculature; transgenic plant; agronomic; longer root;
plant; promoter; tree; crop plant.
                                                                                                                                                                          gene related protein SEQ ID No 17
                                                                                                                                                                                                                                                            Protein;
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Pred. No. 9.2e-31;
7; Mismatches 131
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MINNNINNN----INVNINNNINNNNNNNSHNHHEPQPNYAFTDTSDFSSLDDMNCHLININ

NSNNNNN

NKWNYNNNYYYSPIENSNISKSLEESVLNOFPHNFNLNSSNNNYLNNSSSLHNINQSVNS

LSNNNNNOTNOOPINNNNNNNNNNNNNNNNNNNNN

85

----NDSSSM--VNNMINH

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DNTFFKSNINKMEDNTPKDILYESRNVSNMNGNVLLGLNKNTHHDISTKDENHNDNKINN GN----NNNNITDSPTKSKRHSTYETNIGS-----HQRRKSIQSLIANSAIHSFSKLKNK DKSIFLHKKNLRDN-IKLKNRSSCDNIMNKKKNNLHLARHSVGSKL---TMFSYDPQKNK

NTCGAVNNNSNN-----NNNNNNNST

MN-SINNS-NM

889 319 661 288 601 237 545 197 489 137

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GVINIIN----NSNVNSI-----

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-PLSSSTPSTV

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320 662 289 602 238 546 198 490 138 476

GSLGAIPMDRSFDGNINTITEESTGGNNSPRSNCGSNCGSNGGIPLSPRNLSSLNSGVNV

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                                                                                                                                     The invention relates to an isolated WOODEN LEG (WOL) polypeptide, comprising 15 contiguous amino acids of a fully defined Arabidopsis (CC woODEN LEG protein sequence of 1057 amino acids as given in the specification, and to its encoding nucleic acid. The invention also crelates to an amino acid sequence of domains of protein, e.g., N-terminal CC region, C-terminal domain, etc; or is a naturally occurring allelic covariant of the above mentioned polypeptide sequence. Expression levels of the nucleic acid can be modified to improve the vasculature in transgenic plants and enhance the agronomic properties of such plants. Also the WOL promoter is used to drive expression of a heterologous coding sequence of trees to improve wood production. The WOL nucleic acid may be used as a molecular marker for a qualitative trait loci, e.g., longer roots or cenhanced wood production, in molecular breeding of crop plants. The nucleic acid is also useful in DNA amplification assays to identify the endogenous WOL genes, WOL mutant alleles and/or WOL expression products in cultivars as compared to wild-type plants. They can also be used as condition and in the wOL gene in cultivars and wild-type plants. The CC markers for linkage, analysis of qualitative trait loci. The WOL protein and/or antibodies can be used as diagnostic reagents in immunoassays to detect expression of the WOL gene in cultivars and wild-type plants. The construction is also uncleic acid, and its corresponding antibody are useful for improving agronomically valuable plants e.g., trees. This sequence represents a protein relating to the wooden leg (WOL) protein of
                                                         Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated polypeptide (WOODEN LEG) with ability of asymmetric cell divisions that establish vascular hypocotyl development, useful for improving agronomic
                                                                                                                                                                         sequence represents the invention.
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Benfey PN;
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                                                                                                                                     Sequence
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                                                                             Local
416 TFGKYSSLNDIDKIKKNKKKGLINYKSTLYNDNTINKKHNNNNNNNNNNNDNNNNNNN 475
                                                       al Similarity
242; Conserv
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BONKE A W M.
KAUPPINEN L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Page 151-157; 187pp; English
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                                                                                                                                     2150
                                                           Conservative
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                                                                           9.9%;
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                                                           146;
                                                       Score 676; DB 23;
Pred. No. 1.5e-29;
6; Mismatches 255
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                                                                                              Length 2150;
                                                           Indels 344;
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                                                                                                                                                                                   Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecologic antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
                12-MAR-1999;
                                             08-MAR-2000; 2000WO-US05988
                                                                                                         WO200055174-A1
                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                prostate cancer antigen protein sequence SEQ ID NO:1074.
                                                                                                                                                                    intestinal; pulmonary; infectious disease.
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                99US-0124270
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nephrotropic; antiinfective; gynaecological;
neural; immune; reproductive; renal;
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Best Local S
Matches 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate cancer associated gene sequences, referred cancer antigens, useful for treatment, prevention,
                human
                             Human; mitotic centromere-associated kinesin; NYD-KIF2
                                                             Mitotic
                                                                                           22-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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The prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 1498-1499; 2338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders such as prostate cancer
                                                                                                                        ABB05593;
                                                                                                                                                       ABB05593 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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              genome
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                                                            centromere-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGDIFTFLN--IYDKDNTKGIFISFYEIYCGKLYDLLQKRKMVAALENGKKEVVVKDLK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TASNEVVYRFTARPLVQTIFEGG-KATCFAYGQTGSGKTHTMGGDLSGKAQNASKGIYAM
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Pred. No. 3.7e-30;
9; Mismatches 102;
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                                                            kinesin NYD-KIF2 protein
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RESULT 34
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(1) utilising the NYD-KIF2 gene to prepare a fusion protein;

(2) utilising the NYD-KIF2 gene to prepare and to prepare menoclonal and polyclonal antibodies; and (3) utilising the NYD-KIF2 gene in preparing a testicular specific function gene expressing chip. The expressed protein may become gene medicine for treating related disease. The present sequence represents the human testis mitotic centromere-associated kinesin NYD-YIF2 protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                         AAP60452
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Similarity 44.7%;
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                         standard;
                                                                                                                GK-SKSIMIANISPTISCCEQTLNTLRYSSRVK
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                                                                                                                                                                    AGSERGADTVSQNKQTQTDGANINRSLLALKECIRAMDSDKWHIPFRDSELTKVLRDIFV
                                                                                                                                                                                                         EKEVCCVEEVLNLVEIGNSCRTSRQTSVNAHSSRSHAVFQIILK--SGGIMHGKFSLVDL
                                                                                                                                                                                                                                  ILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNIDLKDINKNTSLGKIAFIDL
                                                                                               GONSSTCMIATISPGMTSCENTLNTLRYANRVK
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                         Protein; 537
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Pred.
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No. 1.
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                                                                                                                                                                                                                                                                                                           Query Match
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11-APR-1985;
11-APR-1985;
11-APR-1986;
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Ag319 of |
                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA
namely t
                                                                                                                                                                                                                                                                                                                                                    The antigens of the invention are prod. using recombinant techniques. They may be used in vaccine compans. to stimul immune response against p.falciparum, the cause of human (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium
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27-JUN-1991
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kemp D
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                                                                                                                                                                                                                                                                                                                                                                                                                               nolecules encoding Plasmodium the SHARP ARP and MESA antigens
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KEMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the Asparagine-Rich Plasmodium falciparum.
                                                                                                                                                                             NIMNKKKNNLHLARHSVGSKLTMFSYDPOKNKDNTFFKSNINKMEDNTPKDILYESRNVS
                            KFYTNYMIKNNLKFNINNNNNNNNNGVFSNRNLINNNNN I NINMNKMIYNYQIRKNSMININM
                                         NMYPNITNNNN----NNNNNNNNNNNNNI DVENYNNRDGTNNSMKLYAYNSHNLFQPDN---
                                                                      MHSRNSNVI--NNYTNOQTRFSSFMMNNNIHFKNKYDNNNNMKGTINNDNNMDY---
                                                                                        ---MNSNSIYKSNYNSNOS----ISDVQIRYVNEMDTSNK----NNDNIFFDAISCDN
                                                                                                                RNNSINIKMG
                                                                                                                                   NMNG-NVLLGLNKNTHHDISTKDENHNDNKINNGVINIINNSNVNSINNSNMNSINNSN-
                                                                                                                                                         NNINEYK----
                                                                                                                                                                                                    ENENK---
                                                                                                                                                                                                                         NNNNSHNNHLPQPNYAFTDTSDFSSLDDMNCHLNNNDKSIFLHKKNLRDNIKLKNRSSCD
                                                                                                                                                                                                                                             YNNNKKNNNNNDDGNMNFKNQYNNNYKFDEEEHLR-----NNSIDMNNSNENEN
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     NKNTSNIQNINTNKNNQDGNVNYSMN-----FCHYNLNDKNYLIDLNNKEQKDKNIHGCD
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(first entry)
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86AU-0056037.
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                                                                                                                ----SQDKNQNSN--NNFYINY---QNTNEFKDNKKNNMNNSNT
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Pred. No. 3.2e
90; Mismatches
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No. 3.2e-26;
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                      The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is Plasmodium falciparum BBP-5 protein.
                                                                                                                                                                                                                                                          New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy; BBP-5.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE29358 standard; Protein; 1331 AA.
                                                                                                                                                                                                                           Claim 27; Page 148-153; 163pp; English.
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1331 AA,
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                                                                                                                                                                                                                                                                                                                                                                    Liu D,
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KYTYPTLSTNEDIYNKEMEGKHIRLDDQDK 10	NQUS ISTNEEPLSNHSINDPGKIKUGIMIUGNULUMNGTQEHSKEEGMUVFEPN	CHADAYSTARRK-NATNINGNIYQADDIIYTINGLADXYSATLLHEKE	NEMKKNEMKNNEMKONHIKSNNINISSSSSSININIYANI INDDTFONDY	MNEW I DOMENNAGE LINGUES DE L'ENVIRONNAGMAN.	NNNNGSHTSIDNMKN 89   III	SI KIEENOSNAEKUUNKUI IEGUMINS KIUKNIGAAI INKSEISINI FENSCHMS VN	MNFCKYNLNDKNYLIDLN		DDDEEEEDDEDDNNNNNDDDNMSDNEEMEDNDEDNDEYNNS 7	1	NEDDNNNNNNDBNCDNNNHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	NKNNDNIFFDA	- IKRCSSNYNYDNNNGYSNESSDNYNNGYNDSTDNNNGYNSNSSYNSNN 619	N-DNKINNGVINIINNSNVNSINNSNVNSINNSNVKS	TLESINPDDHNIFNSEMDSMK-NENNDEEEQTATSIYNILGKIGKDTY- 571	TEFKSNINKMEDNTPKDILY	INNHFNNKDDMI-MKCKNMKGSISMDNNSSNSNSNNTHFEK 52	IKLKNRSSCDNIMNKKKNNLHL	ENIKGMYDNTNQEEMNFNNVSGLLREDNSNMNEIYLTRDNHNNNYHENEENIYSINIKY- 48	25 YANADSSSOMINIANINININININININININININININININININ	DVKKSSSFDIIGSSKNIYEQGENLKNYCIYHNNNFESGFENYILENKQPLELIENHFDIM 42	2	-MANINNANKDIIINRSGISNGNSQSVPCFENILDYDKLKFVEYINSFS 36	TFGKYSS	SVFPYEKFGRHESRNLAIQFSQYEDYMHRIIEDRLYANIQNNLPSVHNMKNMSN- 317	LRYSSRVKNFK	YLGKNINININININIAFSNFVMGNLSSDNISGCFFVEKLNAYLFAMLDKCSNKTVI 26	SDKNHIPFRDSELTKVLRDIFVGKSKSIMIANISPTISCCE		NKNTSLGKI	RRIDNENSDKKESFRTKNKSTIKRSQIDDEDNLQGLLIKE 15	VVVKDLKILRVLTKEELILKMIDGVLLRKIGVNSQNDESSRSHAILNI	YVSSDLLNFLKCYSNLNINLNKVPYDLVYSFLLDGELYLGYDISVFILLVKAEHFEYC 109	GDIFTFLNIYDKDNTKGIFISFYEIYCG	); Conservative 180; Mismatches 412; Indels 512; Gaps 6

nucleotide

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                   The present invention describes proteins and their fragments (I) encored by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (I) vaccines against P. falciparum infection comprising (I) or (II) (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal
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antimalarial; malaria;
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                                                                                                                                                                      Disclosure; Page 75-82;
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                          DNIYDQGNIKKNEEEITKHDEYISREEKNKYNSKCIRNFDDYKYEQVLSYHTLDEDKKKN
                                                                    DNTFFKSNINKMEDNTPKDILYESRNVSN-MNGNVLLGLNKNTHHDI---STKDENHNDN
                                                                                                                                                   KKNLRDNI-KLKNRSSCDNIMNKKKN------NLHLARHSVGSKLTMFSYDPQKNK
                                                                                                                                                                                               FKVSLKEKKYIDNISNNMERVTYKNEM--INEKISKMDDILYPCDKNKSLNMSCPVI---
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497 817 458 766 410 357 657 310 616

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SEQ

ID NO:173

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RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CC by.chromosome 2 of the human malarial parasite, Plasmodium falciparum.

CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2)

CC vaccines against P; falciparum infection comprising (I) or (II);

CC (I) and (II) are useful for the development of vaccines against

CC P; falciparum infection. (I) and polyclonal antisera or a monoclonal

CC antibody raised to immunogens comprising the sequences of (I), are

CC (I) especially when they are rifins or secreted or membrane proteins)

CC (I) (especially when they are rifins or secreted or membrane proteins)

CC an aid the identification of drugs to treat or prevent P; falciparum

CC (I) (especially when they are rifins or secreted or membrane proteins)

CC can aid the identification of froteins treat or prevent P; falciparum

CC P; falciparum. Sequencing of the Plasmodium chromosome 2 and the

CC subsequent identification of proteins encoded by it will help to expand

CC our understanding of parasite biology, a process hampered by the

CC complexity of the parasitic lifecycle, and provide new targets for

CC vaccine and drug development. Parasite resistance to drugs and mosquito

CC resistance to insecticides have led to a resurgence of malaria in many

CC parts of the world, and there is a pressing need for vaccines and new

CC drugs. AAA70078 to AAA70287 and AAB18352 represent nucleotide

CC and protein sequences given in the present invention, but which are not

CC specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                       Matches 302;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum; antimalaria; malaria;
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(GARD/)
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) CARUCCI D.
) GARDNER M.
) VENTER J C.
                                                                                     NYFKNL----FNLNDVSNNKVINIIEQKEGDERNADN----NLKNKNIVRDNINKIKN
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protozoacide; infection; insecticide.
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                                        KKYINEDIKUMSLEEIDKTAQSIYEKRKVLLTKLLLLFKKNVDTQINNETSDLRKDLVMC 1195
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                                                                                  MNSFEIELYLKINNDIFLQFNKHNYNVQNFYNFSITLIN--IMSKYYSENFYAYNLEKIV
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                                                      (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB1832 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against p. falciparum infection comprising (I) or (II) (I) and (II) are useful for the development of vaccines against p. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with p. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins encoded by chromosome 2 of the human Plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection -
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antimalarial; malaria; protozoacide; infection; insecticide.
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) CARUCCI
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                                                                                                                VIKSKPLVDNPLDDEHIYS-EHLNNRILNDETLPSAQLNVETL----YGEHEYNEQRMN
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                                                                                                                                                                                                                                                                                       ----EEIDKTAQSIYEKRKVLLTKLLLLFKKNVDTQINNETSDLR--KDLVMCHICNN--
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Matches 159;
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(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins AAW02657-W02720 represent a range of G-protein coupled receptor (GPR) proteins selected from CAMP, adenosine, muscarinic acetylcholine, adrengergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin, opsin, cytomegaloviral and other GPR proteins. The peptides
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10-SEP-1992;
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                        The
                                                              Disclosure; Page 177-182; 577pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium
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                                                                                                         Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                             WPI; 2000-365347/31.
                                                                                                                                                                                                                                        Hoffman S,
                                                                                                                                                                                                                                                                                                      (HOFF/)
(CARU/)
(GARD/)
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e present invention describes proteins and their fragments (I) encoc
chromosome 2 of the human malarial parasite, Plasmodium falciparum.
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CARUCCI D.
GARDNER M.
VENTER J C.
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protozoacide; infection;
                                                                                                                                                                                                                                        Gardner M,
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                                                                                                                                                                                                                                        Venter JC;
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CC (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal CC antibody raised to immunogens comprising the sequences of (I), are CC useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the CC usefuent identification of proteins encoded by it will help to expand CC ur understanding of parasite biology, a process hampered by the CC complexity of the parasitic lifecycle, and provide new targets for CC vaccine and drug development. Parasite resistance to drugs and mosquito CC parts of the world, and there is a pressing need for vaccines and new CC parts of the vorld, and there is a pressing need for vaccines and new CC and protein sequences given in the present invention, but which are not cx specifically mentioned within the specification.
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Matches 28
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                                                                                         APVKNYIIGENLCGENGCGKNGCGDILRGDILCGDILRGDNNSIPLFRSNRIFCKQS---
                                                                                                                                 NGVINI INNSNVNS INNSNMN--
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        -YIYFNKILKRLQSLD-DMY---
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Search completed: October 2, 2003, 16:17:06 Job time: 105 secs

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asparagine-rich protein (clone 52C11) - C;Species: Plasmodium falciparum C;Date: 31-Dec-1991 #sequence_revision 3 C;Accession: $14508 R;Schreiber, L.; Deutsche, U.; Storck, T submitted to the EMBL Data Library, Dece
                                                                                                                                                                              RESULT 2
S14508
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A; Residues: 1-391 <SCH>
A; Cross-references: EMBL: X174
C; Superfamily: Saccharomyces
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A;Accession: S14577
A;Status: preliminary
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                                                                                   A; Molecule type: mRNA
A; Residues: 1-419 < SCH>
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A; Accession: S14508
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                                                                                                                                 T.; Mueller-Hill,
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                                                                                                                                                                                                                                                                                                                                                                                                            malaria parasite (Plasmodium falciparum)
                                                                                                                                                                      Plasmodium
                                                                         PID:g9855
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A;Cross-references: EMBL:Z35845; NID:g536135; PIDN:CAA84905.1; PID:g536136; MIPS:YBL084 A;Experimental source: strain S288C

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S45925

Cell division control protein CDC27 - yeast (Saccharomyce N;Alternate names: protein YBL0718; protein YBL084c C:Species: Saccharomyces cerevisiae C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_C;Accession: 945825; S45422; S28742; S59219 R;Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, submitted to the Protein Sequence Database, August 1994 A;Reference number: S45816 A;Accession: S45825
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R;Zhao, Y.; Kappes, B.; Yang, J.; Franklin, R.M.
Eur. J. Biochem. 207, 305-313, 1992
A;Title: Molecular cloning, stage-specific expre
A;Reference number: S23466; MUID: 92331669; PMID:
A;Accession: S23467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-666 <DIE>
A;Cross-references: EMBL:U18530; NID:g602367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, December 1994 A,Description: Saccharomyces cerevisiae chromosome A,Reference number: S50428 A;Accession: S50452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S
R; Dietrich, F.
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S50452
A; Molecule type: DNA
A; Residues: 1-758 < DOM>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X63648; NID:g9937; PID:g9939
C;Superfamily: human long-chain-fatty-acid-CoA ligase;
C;Superfamiles: acid-thiol ligase; coenzyme A
C;Keywords: acid-thiol ligase; coenzyme ACL>
F;103-732/Domain: acetate-CoA ligase homology <ACL>
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A; Residues: 1-749 < ZHA>
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A; Map position:
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                                                                                                                                                                                                                                                                                                                                               287
                                                                                                                                                                                                                                                                                                                                                                                       758
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1.3e-07;
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C;Accession: S68824
R;Kawata, T.; Steel, J.B.; Williams, J.G.
FEBS Lett. 386, 103-109, 1996
                                                                                                                                                                                                                                                                                                                                                                           rngB protein, cytosolic - slime mold (Dictyostelium discoideum)
N;Alternate names: RING finger protein
C;Species: Dictyostelium discoideum
C;Species: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;642-675/Domain: tetratricopeptide F;676-709/Domain: tetratricopeptide F;710-743/Domain: tetratricopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2L C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat ho C;Keywords: nucleus C;Keywords: nucleus F;472-505/Domain: tetratricopeptide repeat homology <TT1>
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                                                                        a C C
                                                                                                                                                            A;Experimental source: maturing cells
C;Genetics:
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A; Residues: 1-943 < KAW>
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A; Residues: 442-691 <OBW>
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A;Residues: 607-619 <SIK>
R;Obermaier, B.; Gassenhul
Yeast 11, 1103-1112, 1995
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A;Accession: S28742
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A;Description: Sequence analysis of a 78,6 kb segment of the left end
                                                                                                                                                                                                                                               A; Accession: S68824
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Best Local S
Matches 17
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                                                                                   Superfamily: RING finger homology
                                                                                                                                                                                                                                                                    ;Title: RNGB: a Dictyostelium RING finger;Reference number: S68824; MUID:96228044;
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  Query Match
Best Local
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                                                              -937/Domain: RING finger homology <RNG>
  Local Similarity
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t homology <TT4>
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t homology <TT7>
t homology <TT7>
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PMID:8647262
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DB 2; L
1.8e-07;
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                       Length 943;
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RESULT S57698

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A;Atatus: pre....
A;Status: pre....
A;Molecule type: DNA
A;Molecule type: DNA
Cances: 1-1093 <ZHO>
Cances: EMBL:U23479;
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A;Residues: 1-1139 <ALE>
A;Cross-references: EMBL:U50042; NID:g1399511; PIDN:AAC47162.1; PID:g1399512
R;Sydow, L.; Alexander, H.; Alexander, S.
submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S71092; S21443
R;Alexander, H; Lee, S.K.; Yu, S.L.; Alexander, S.
Nucleic Acids Res. 24, 2295-2301, 1996
A;Title: repE-The Dictyostelium homolog of the human xeroderma
A;Reference number: S71092; MUID:96279729; PMID:8710499
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T18275
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C; Superfam
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Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 4 - C;Species: Dictyostelium discoideum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 860-1139 <SYD>
                                                                                                                                                                                                                                                                             A;Reference number: S21443
A;Accession: S21443
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C;Keywords: phosphotransferase
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A; Accession: T18275
                                                                                                                                                                                   A;Gene: repE
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic
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Pred. No.
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                                                                      Mismatches
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2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                              not
                                                                                     2.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                         Length 1139;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-39,41-78,80-119,121-159,161-199,201-230,232-279,281-282,'L',284-319,321-35
79,881-892,'M',894-919,922-960,962-1000,1002-1040,1042-1080,1082-1103,'L',1105-1120,1122
R;van der Aart, Q,J.M.; Steensma, H.Y.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64541
A;Accession: S64557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: Strain Gar. C.W.
R;Creasy, C.L.; Madden, S.L.; Bergman, L.W.
Nucleic Acids Res. 21, 1975-1982, 1993
A;Title: Molecular analysis of the PHO81 gene of Saccharomyces
A;Title: Molecular analysis of the PHO81 gene of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory protein PHO81 - yeast N; Alternate names: protein 1178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1178 <VAN>
A;Residues: 1-1178 <VAN>
A;Cross-references: EMBL:Z73018; NID:g1323420; PID:g1323421; MIPS:YGR233c
A;Cross-references: EMBL:Z73018; NID:g1323420; PID:g1323421; MIPS:YGR233c
A;Cross-references: EMBL:Z73018; NID:g1323420; PID:g1323421; MIPS:YGR233c
A;Cross-references: EMBL:Z73018; NID:g1323420; PID:g1323421; MIPS:YGR233c
A;Cross-references: CANANA
A;Cross-references: S6396; MUID:g6267763; PMID:g701610
A;Accession: S63914
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acta Biochim. Biophys. Sin. 26, 283-287, 1994
A;Title: Conformation prediction and function
A;Reference number: JC1032
A;Accession: JC1032
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Nucleic Acids Res.
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A;Description: Sequence analysis of the 43 KB CRM1-YLM9-PET54-SMI1-PHO81-YHB4-PFK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1178 <
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                                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                                        A; Cross-references: SGD: S0003465; MIPS: YGR233c
                                                                                                                                                                                                                                                                                                                                       A; Gene: SGD: PHO81
                                                                                                                                                                                                                                                                                                                                                                                        A; Note: the nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Wu,
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A; Residues: 1-1178 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Status: not compared with conceptual translation;Molecule type: DNA;Residues; 1-10 <CRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: Nucleotide sequence of the PHO81 gene involved Reference number: S20136; MUID:90245670; PMID:2186378; Accession: S20136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Residues: 1-918,920-1178 <COC>;Cross-references: EMBL:X52482; NID:g4139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Mar-2001;Accession: S57698; S20136; S41074; JC1032; S64557; S63914;Van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: translation not shown
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Accession: S57698
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                                                                                                                                                                   ;330-346/Domain: transmembrane #status predicted;904-920/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X87941; NID:g886908; Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:S61041; NID:g385415; PIDN:AAD13922.1; Wu, J.S.; AO, S.Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
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                                                         Matches
                                                                                                                                                                                                330-346/Domain:
                                                                                                                                                                                                                                                 Superfamily: ankyrin; ankyrin repeat homology
                                                      Local Similarity
nes 17; Conserv
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Acids Res. 18, 2176, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                               1-1178 <VAF>
                                                         Conservative
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                                                                                   100.0%;
                                                                                                                   1.3%;
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                                                                                      Score 17;
Pred. No.
                                                         Mismatches
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                                                                                      2.1e-07
                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA61183.1;
to the EMBL Data
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                                                                                                                                                                      <TM1 >
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                                                                                                             Length 1178;
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Library, Ju
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submitted to the EMBL Data Library, January 1998 A;Description: YakA, a protein kinase required for Reference number: Z18146
                                                                                                                                                                                                                                                                                                                                                protein kinase YakA (EC 2.7.1.-) - slime mold (Dictyostelium discoideum) C;Species: Dictyostelium discoideum C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text change 20-Sep-1
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
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A; Residues: 1-1338 < ADL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1996 A; Reference number: Z18856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Adler, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T18287
                                                                                                                              C; Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific
                                                                                                                                                                                                                                                                                                                      R;Kuspa,
                                                                                                                                                                                                                                                                                                                                    C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                          T14577
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                    A;Status:
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                                                                                                                                                                                                 1;Residues: 1-1457 <KUS>
                                                                                                                                                                   ;Genetics
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                                                                                              Query Match
                                                                                                                                                   yakA
                                                                                                                                                                                                                                                                                                                      A.; Lu, S.; Souza,
                                                                                                                                                                                                                             preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
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                             741 TNNNNNNNNNNNNNNN 757
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                                                                                  Similarity
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                                                                Conservative
                                                                                                                                                                                  EMBL: AF045453;
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                                                                              1.3%; Score 17;
100.0%; Pred. No.
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60
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Pred. No.
                                                                                                                                                                                 NID:g2854116; PID:g2854117; PIDN:AAC02554.1
                                                                  Mismatches
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2.4e-07;
                                                                                DB 2; Lt
2.5e-07;
                                                                                                                                                                                                                                                                                        for
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                                                                                                Length 1457;
                                                                                                                                                                                                                                                                                       growth
                                                                  Indels
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                                                                  Gaps
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                                                                  0
                                                                                                                                     protein
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742 NNNNNNNNNNNNNNN 758
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RESULT 12 S71628

R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; EMBO J. 15, 3880-3889, 1996 A;Title: The hybrid histidine kinase Doka A;Reference number: S71628; MUID:96324396;

MUID:96324396;

is part of the ; PMID:8670893 Gerisch,

A;Status: nucleic a A;Molecule type: DN A;Residues: 1-1670

DNA

acid sequence <SCH>

not shown

A;Accession: S71628

sensory transduction histidine kinase dokA - slime mold (Dictyostelium discoideum) C;Species: Dictyostelium discoideum C;Date: 27-Nov-1997 #sequence\_revision 12-Dec-1997 #text\_change 11-Jan-2002 C;Accession: S71628; S78068

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G.;

Simon, osmotic

3

response system

O.F Dic

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κ;zında, M.J.; Singleton, C.K.
Dev. Biol. 196, 171-183, 1998
A,Title: The hybrid histidine kinase dhkB regulates spore
A;Reference number: Z16506; MUID:98248997; PMID:9576830
A;Accession: T08875
                                                                                       hypothetical protein C0425w - malaria parasite C;Species: Plasmodium falciparum C;Jate: 15-Oct-1999 #sequence_revision 15-Oct-1: C;Accession: T18440 R;Lawson, D.; Bowman, S.; Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X96869; NID:g1237201; PID C;Genetics:
A;Genetics:
A;Genetics:
A;Geneticn:
A;Description:
modulates cell response to changes C;Superfamily: response regulator homology C;Keywords: phosphoprotein; signal transduction F;1520-1629/Domain: response regulator homology <R F;1568/Binding site: phosphate (Asp) (covalent) #s
                                                                                                                                                                                    RESULT 14
T18440
                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 790/3
C;Superfamily: response regulator homology
C;Keywords: protein kinase; transmembrane protei
F;1841-1964/Domain: response regulator homology
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A;Experimental source: strain KAx3
C;Genetics:
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A;Experimental source: strain AX2; substrain 214

A;Experimental source: strain AX2; substrain 214

R;Schuster, S.C.; Noesel, A.A.; Oehme, F.; Gerisch, submitted to the EMBL Data Library, March 1996

A;Description: The hybrid histidine kinase DokA is 1
               A;Accession: T18440
A;Status: prelimina
                                                                     R;Lawson, D.; Bowman, S.; Barrell, submitted to the EMBL Data Library,
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A; Residues: 1-1969 <SIN>
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R;Zinda, M.J.; Sing
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                                                    A; Reference number: Z18935
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               Status: preliminary; translated
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erences: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1;
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Query Match
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A;Cross-references: EMBL:AC004521; NID:g3128166; PID:g3128179
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                          C;Accession: S05356
R;Shaw, D.R.; Richter, H.; Giorda, I
Mol. Gen. Genet. 218, 453-459, 1989
                                                                                                                                                                                       hypothetical protein (clone pLK330) - slime mold () C;Species: Dictyostelium discoideum C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2944340 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F4I1.15 C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                  A; Title: Nucleotide sequences of Dictyostelium discoideum A; Reference number: S05355; MUID:90066348; PMID:2511421
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C; Superfamily:
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A; Residues: 1-188 < STO>
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A; Note: C0425w
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A; Residues: 1-317 < SHA>
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A; Residues: 1-188 < ROU>
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A; Map positi
C; Keywords:
hypothetical protein G2 - slime mold (Dictyostelium discoideum) C;Species: Dictyostelium discoideum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T18285; S28720 C;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, Genetics 148, 1117-1125, 1998
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Proc. Natl. Acad. Sci. U.S.A. 94, 7685-7690, 1997
A;Title: A maize zinc-finger protein binds the prolamin
A;Reference number: Z14511; MUID:97352860; PMID:9207153
A;Accession: T02046
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A;Experimental source: cultivar Landsberg erecta; inflorescence
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C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
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A; Residues: 1-328 < VIC>
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                K.J.; Kiyosawa,
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A;Cross-references: EMBL:Z48952;
A;Experimental source: strain ABS
                               A; Molecule type: DNA
A; Residues: 1-490 < PEA>
                                                                                             R; Pearson, D.; Bowman, S. submitted to the EMBL Data
                                                                                                                                        C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 29-Oct-1999
                                                                                                                                                                         HMS1 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YM9916.09; protein Y
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                                                                             A; Reference number:
                                                                                                                              C; Accession: S52830; S59820
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A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Acc
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                                                                                                                                                                                                                                                                A, Title: Identification and targeted gene disruption of A, Reference number: A46391; MUID:93170666; PMID:8382181 A, Accession: A46391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Johnson, R.L.; Saxe III, C.L.;
Genes Dev. 7, 273-282, 1993
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C;Date: 18-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 29-Oct-1999
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NID: 9763008; PIDN: CAA88795.1; PID: 9763017; MIPS: YMR070

April

1995

protein YMR070w

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A;Cross-references: GB:Z97344; NID:g2245126; PIDN:CAB10555.1; PID:g2245134 R;Hubbel, A.; Schoeffl, F.
Plant Mol. Biol. 26, 353-362, 1994
A;Title: Arabidopsis heat shock factor: isolation and characterization of A;Reference number: S52641; MUID:95036006; PMID:7948881
A;Accession: S52641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzis, N.
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A;Reference number: A71400; MUID:98121113; PMID:9461215
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A; Variety: columbia

C; Date: 01-Aug-1995 #sequence revision 24-Mar-1999 #text_change 16-Jun-2000

C; Date: 01-Aug-1995 #sequence revision 24-Mar-1999 #text_change 16-Jun-2000

C; Accession: F71447; S52641; S62227; S38873

R; Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.;

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.;

P.; Wedler, H.; Wedler, P.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk,

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Puigdome

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Puigdome
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A;Map
                                                                                                                                                                                                                                                                                                                                                                           A; Description: Arabidopsis A; Reference number: S38873
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A;Residues: 31-215,'M',217-284,'D',286-335,'T',337-389,'Y',391-469,474-495
R;Huebel, A, Schoeffl, F.
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-215,'M',217-284,'D',286-335,'T',337-389,'Y',391-469,474-495
A;Cross-references: EMBL:X76167
A;Accession: S62227
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A; Residues: 1-495 <BEV>
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A;Cross-references: MIPS:YMR070w;
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A; Residues: 1-490 < MAD>
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                                         ;Description: transcription factor that binds to heat shock promoter elements ;Superfamily: tomato heat shock transcription factor HSF8; HSF DNA-binding domain homol; Reywords: DNA binding; heat shock; leucine zipper; nucleus; stress-induced protein; tr;53-148/Domain: HSF DNA-binding domain homology <HSF>;53-148/Domain: HSF DNA-binding domain homology <HSF>;181-202/Region: leucine zipper
                                                                                                                                                               Function: <TFC>
                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
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  Query Match
                                                                                                                                                                                                                                         Gene: HSF1
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                                                                                                                                                                                                                                                                                  Cross-references:
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                                                                                                                                                                                                                                                                                                                                                          Accession: S38873
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16; Conserv
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erences: EMBL:X76167;
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NID:g429154; PIDN:CAA53761.1; PID:g429155
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                        R;Lawson,
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RESULT 25
T18446
T18476
hypothetical protein MAL3P3.11 -
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T18446
                                                                                                                                                                                                                                                                                                                                                                                                            R;Lawson, D.; Bowman, S.; Barrell, submitted to the EMBL Data Library, A;Reference number: Z18935
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A;Title: Developmental regulation of DEAD box proteins A;Reference number: S53813; MUID:95209781; PMID:7695838
A;Accession: S53813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA helicase - slime mold (Dictyostelium discoideum C;Species: Dictyostelium discoideum C;Date: 15-U1-1995 #sequence_revision 23-Aug-1997 C;Date: 15-U1-1995 #sequence_revision 23-Aug-1997
                                                                                                                                                                                                                                                                              A; Map position: 3
A; Introns: 437/3;
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A; Residues: 1-580 < LAW >
                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: T18439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C0380w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S53813; R; Mahal, B.; Nellen,
                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
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A; Residues: 1-566 < MAH >
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S.; Barrell, | Data Library,

August 1997

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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: A71607
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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A; Introns: 437/3;
A; Note: MAL3P3.11
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A;Accession: T18446
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross.references: GB:AE001416;
A;Experimental source: clone 3D7
C;Genetics:
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A; Residues: 1-600 < LAW >
                                                                                                                                       A; Experimental source: C; Genetics:
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C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: A71607
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A; Introns: 534/2;
                                                                                                                   A; Gene: NCSP:B7J19.60
                                                                                                                                                     A;Cross-references: EMBL:AL389899; GSPDB:GN00116; NCSP:B7J19.60
A;Experimental source: BAC clone B7J19; strain OR74A
                                                                                                                                                                                                                A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                    A; Reference number: Z25286
A; Accession: T51007
                                                                                                                                                                                                                                                                                                                                 hypothetical protein B7J19.60 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C;Accession: T51007
                                                                                                                                                                                                A;Residues: 1-720 <SCH>
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Local Similarity 100.0%;
hes 16; Conservative (
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Pred. No.
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J. 1.2e-06;
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hes 0;
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                                      Length 720;
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A;Reference number: Z16451
A;Accession: T08605
A;Status: preliminary; tra
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RESULT 29
T08611
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A;Molecule type: DNA
A;Molecule type: HUNs
A;Residues: 1-758 <HUNs
A;Cross-references: GB:Z49705; EMBL:Z49700; NID:g825556; PIDN:CAA89800.1; PID:g825569;
A;Cross-references: GB:Z49705; EMBL:Z49700; NID:g82556; PIDN:CAA89800.1; PID:g825569;
                                                                                                                                                                                                                                                                                                                                        hypothetical protein DocA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 1
C;Date: 11-Jun-1999
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C;Date: 08-011-1995 #sequence_revision 01-Sep-1995
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                                                                                                                                        A;Gene:
                                                                                                                                                                          A;Cross-references: EMBL:AF020409; NID:g2425146; PID:g2425147
A;Experimental source: strain AX4
                                                                                                                                                                                                                                                                                             submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                            R; Aubry, L.; Firtel, R.A.;
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Similarity 100.0%;
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ITNNNNNNNNNNNN 179
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100.0%; Pred. No. 1.3e-06;
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Pred. No.
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hypothetical protein HelE - slime mold (Dictyostelium discoideum) (fragment) C;Species: Dictyostelium discoideum C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999 C;Accession: T08605
R;Loomis, W.F.; Iraniar, N. submitted to the EMBL Data Library,
                                                                                                                                                                                           T08605
                                      ₩.F.;
                                      Iranfar, N
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A; Molecule type: DNA

translated from GB/EMBL/DDBJ

August

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A;Map position: 4L
C;Keywords: transmembrane protein
C;Keywords: transmembrane #status predicted <TM1>
F;52-73/Domain: transmembrane #status predicted <TM2>
F;92-108/Domain: transmembrane #status predicted <TM2>
F;140-156/Domain: transmembrane #status predicted <TM3>
F;181-197/Domain: transmembrane #status predicted <TM5>
F;623-639/Domain: transmembrane #status predicted <TM6>
F;623-639/Domain: transmembrane #status predicted <TM6>
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A;Gene: SGD:GPR1; gpr1
A;Cross-references: SGD:S0002193
F;56-74/Domain: transmembrane #status predicted <TM1>
F;91-109/Domain: transmembrane #status predicted <TM2:
F;139-157/Domain: transmembrane #status predicted <TM:
                                                                                                                                                                               A;Accession: JC5808
A;Status: nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-962 <YUN>
C;Comment: This protein monitors
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Saccharomyces cerevisiae
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 19-Apr-2
C;Date: 05-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 19-Apr-2
C;Accession: JC5808
R;Yun, C.W.; Tamaki, H.; Nakayama, R.; Yamamoto, K.; Kumagai, H.
Biochem. Biophys. Res. Commun. 240, 287-292, 1997
A;Title: G-protein coupled receptor from yeast Saccharomyces cerevisiae.
A;Reference number: JC5808; MUID:98049822; PMID:9388468
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C;Date: 12-Jul-1996 #sequence_revis:
C;Accession: S67568
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A; Residues: 1-961 < P.
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C;Species: Saccharomucon control
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A; Cross-references: EMB
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Matches 16
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Date: 04-Feb-1998 #sequence_revision l3-Mar-1998 #text_change 19-Apr-2002
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;Experimental source: strain S288C
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Pred. No.
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Pred. No. 1.6e-06;
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RESULT 34
S54067
A;Map position: 16R
C;Keywords: transmembrane protein
F;711-727/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 26-Jul-1996 #text_change 19-Apr-2002
C;Accession: S54067; S61063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: unassigned GAL4-type zinc cluster proteins; G;Keywords: DNA binding; nucleus; transcription regulation; F;16-52/Domain: GAL4 zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster homology GAL4-zinc binuclear cluster binuclear cluster homology GAL4-zinc binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear cluster binuclear clu
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C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
C;Accession: S48404
                                                                                                                                                                            A;Cross-references: EMBL:Z68111; MIPS:YPR042c C;Genetics:
                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 465-1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Badcock, K.; Churcher, C.M. submitted to the EMBL Data Library,
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                                                                                                      A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-508 <BAD>
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A; Residues: 1-964 < CHU>
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es 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <TM5>
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C;Species: Dictyostelium discoideum
C;Date: 11-Uun-1999 #sequence_revision 11-Jun-1999
C;Accession: T09057
R;Singleton, C.K.; Mykytka, B.; Zinda, M.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z16542
A;Accession: T09057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 36
S14556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable protein-histidine kinase (EC N;Alternate names: histidine kinase C
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hypothetical protein DG2033 - slime mold (Dictyostelium discoideum) (fragment) C;Species: Dictyostelium discoideum C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 4
C;Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1225 <SIN>
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                                                                                                                            В
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                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 'Q',210-1251,'NEENDETALDTIIQPPIKKKK' <8C2>
A;Cross-references: EMBL:X17488; NID:g9852; PID:g9853
                                                                                                                                                                                                                                                                                                                          A;Accession: S14548
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A;Reference number: S14469
A;Accession: S14556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asparagine-rich protein (clone 18C1) - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 20-Feb-195 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000 C;Date: 20-Feb-195 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000 C;Accession: S14566; S14548
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                                                                        RESULT 37
                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-1256 <SCH>
A;Cross-references: EMBL:X17485; NID:g9846; PID:g1335715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                       T08607
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Best Local S
Matches 16
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Best Local Similarity
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Best Local
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ilarity 100.0%;
Conservative
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100.0%; Pr
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100.0%; Pred. No.
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Pred. No. 1.8e-06
0; Mismatches 0
                                                                                                                                                                                                   Pred. No. 2.1
; Mismatches
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R;Loomis, W.F.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z18857
A;Accession: T18288
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status, P. DNA
A; Molecule type: DNA
A; Residues: 1-1271 < LOO>
A; Cross-references: EMBL: AF020282;
A; Cross-references: emBL: AF020282;
                                                                                                                                                                                                                                                                                                               R.Brunk, B.P.; Adler, P.N.
R.Brunk, B.P.; Adler, P.N.
submitted to the EMBL Data Library, November 1990
A.Description: The Drosophila regulatory gene supplies.
A:Reference number: S14871
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S14871
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A;Reference number: Z16451
A;Accession: T08607
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-612,614-784,'N',786-830,'R',832-965,967-1064,'E',1066-1096,'N',1097-1286, A;Cross-references: EMBL:X56798; NID:g8526; PIDN:CAA40134.1; PID:g8527 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990 C;Genetics:
                                                                                                                           R;Brunk, B.D.; Adler, P.N.

Nucleic Acids Res. 19, 3149, 1991
A;Title: The sequence of the Drosophila regulatory gene Suppressor two A;Reference number: $16845, MUID:91279476; PMID:2057369
A;Accession: $16845
                                                                                                                                                                                                                                                                                                                                                                                                               suppressor two of zeste protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S14871; S16845
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T18288
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A;Residues: 1-1365 <BRU>
A;Cross-references: EMBL;X56799; NID:g8528; PID:g8529
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A; Residues: 1-1336 <LOO>
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                                                                                                              A;Status: nucleic acid sequence not shown;
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Best Local Similarity
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                 regulatory gene suppressor
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o. 2.2e-06;
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2.1e-06;
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trfA protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14004
R;Saito, J.; Adachi, H.; Sutoh, K.
J. Biol. Chem. 273, 24654-24659, 1998
A;Title: Dictyostelium TRFA homologous to yeast Ssn6 is required for normal growth and A;Reference number: Z17852; MUID:98406112; PMID:9733762
A;Accession: T14004
A;Accession: T14004
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T14004
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A;Cross-references: FlyBase:FBgn0008654
A;Introns: 55/1; 139/2; 219/3
C;Superfamily: Drosophila suppressor protein of zeste; RING finger homology C;Keywords: DNA binding; nucleus; zinc finger
C;Keywords: DNA binding; nucleus; zinc finger
Search completed: October 2, 2003, 16:36:14 Job time: 78 secs
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A;Gene: trfA
A;Introns: 333/3; 364/3; 637/1
                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues; 1-1390 <SAI>
A;Cross-references: EMBL:AB009080; NID:d1228566; PID:d1034109; PIDN:BAA33143.1
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"The nucleotide sequence of Saccharomyces cerevisiae chromosome Nature 387:78-81(1997).
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CDC27 OR SNB1 OR YBL084C OR YBL0718.
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Lamb J.R., Michaud W.A., Sikorski
"Cdc16p, Cdc23p and Cdc27p form a
EMBO J. 13:4321-4328(1994).
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SUBUNIT: CDC16, CDC23 AND CDC27 FORMS A MACRO SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE CDC27/NUC2 FAMILY.
SIMILARITY: Contains 8 TPR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins as essential components of the yeast cell cycle."; Spring Harb. Symp. Quant. Biol. 56:663-673(1991).
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PubMed=1819514;
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RESULT 3
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphatidylinosicol 4-kinase (EC 2.7.1.67) ()
kinase) (PI4K-alpha).
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P54677;
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DOMAIN
                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: ACTS ON PHOSPHATIDYLINOSITOL (PI) IN THE FIRST COMMITTED STEP IN THE PRODUCTION OF THE SECOND MESSENGER INOSITOL-1,4,5,-TRISPHOSPHATE.
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = 1-phosphatidyl-1D-myo-inositol 4-phosphate.
-!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: biological roles of putative mammalian p110 and yeast Vps14p PI 3-kinase homologs during growth and development."; Mol. Cell. Biol. 15:5645-5656(1995).
                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
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InterPro; IPR000403; PI3_PI4_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96009592; PubMed=7565716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=AX3;
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                                                                                                                                                                                                                                 PF00454; PI3_PI4_kinase; SM00146; PI3Kc; 1.
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             Similarity
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PS00916; PI3 4 KINASE 2;
PS50290; PI3 4 KINASE 3;
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4_KINASE 3; 1.
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                                          8762BC78355AA635 CRC64;
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use by non-profit institutions as long as modified and this statement is not removed. It entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: UNDER LOW-PHOSPHATE CONDITION PHO81 INHIBITS THE KIN ACTIVITY OF THE PHO80 (CYCLLN)-PHO85 (KINASE) COMPLEX.
-i- SUBUNIT: ASSOCIATES SPECIFICALLY WITH THE PHO80-PHO85 COMPLEX, MUCH OF THIS INTERACTION IS MEDIATED THROUGH THE PHO80 CYCLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95025879; PubMed=7939631; Schneider K.R., Smith R.L., O'Shea "Phosphate-regulated inactivation company in the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company 
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van der Aart Q.J.M., Kleine K., Steensma H.Y.;
"Sequence analysis of the 43 kb CRM1-YLM9-PET54-DIE2-SMI1-PHO81-YHB4-
PFK1 region from the right arm of Saccharomyces cerevisiae chromosome
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Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
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MEDLINE=93261834; PubMed=8493108;
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Ogawa N., Noguchi K.-I., Y
Yoshida K., Oshima Y.;
"Promoter analysis of the
                                                                                                                                                                                                                                                                                     SUBUNIT.
-!- SIMILARITY: Contains 6 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 266:122-126(1994).
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Coche T., Prozzi D., Legrain M., Hilger F., Vandenhaute J.;
Coche T., Prozzi D., Legrain M., Hilger F., Vandenhaute J.;
"Nucleotide sequence of the PHO81 gene involved in the regulation the repressible acid phosphatase gene in Saccharomyces cerevisiae.
Nucleic Acids Res. 18:2176-2176(1990).
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16-OCT-2001 (Rel. 40, Last annotation update)
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K.-I., Yamashita Y.,
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n the phosphatase regulon of Saccharomyces
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AAC4_DICDI
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                                                                                                                                                                                                                                       ul-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
AAC-rich mRNA clone PLK330 protein (Fragment).
Dictyostelium discoideum (81ime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI TaxID-44689;
                                                                                                                                                                                                                                                                                             P14198;
01-JAN-1990 (Rel. 13, 0
01-JAN-1990 (Rel. 13, 1
01-FEB-1994 (Rel. 28, 1
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                               asparagine, glutamine, or threonine.";

Mol. Gen. Genet. 218:453-459(1989).

-i- DEVELOPMENTAL STAGE: THE CONCENTRATION OF AAC-RICH MENAS IS IN DORMANT SPORES AND GROWING CELLS, BUT INCREASES DURING SPORE-GERMINATION AND MULTICELLULAR DEVELOPMENT.

-i- MISCELLANEOUS: SEVERAL PROTEINS DERIVE FROM AAC-RICH MENA, DUE TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS INCREASED TO A FRAMESHIFT ALSO HAVE ACA AND CAA CODONS AND THUS INCREASED.
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PROSITE; PS50088; ANK_REPEAT; 2.

PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00023; ank; 6. Pfam; PF03105; SPX; 1. SMART; SM00248; ANK; 3.
                                                                                                                                                          Shaw D.R., Richter H., Giorda R., Ohmachi T., Ennis H.L.; "Nucleotide sequences of Dictyostelium discoideum developmentally regulated coDNAs rich in (AAC) imply proteins that contain clusters asparagine, glutamine, or threonine.";
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                                                                                                                                                                                                         MEDLINE=90066348; PubMed=2511421;
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; D13228; BAA02508.1;

; X87941; CAA61183.1;

; Z73018; CAA97261.1;

; Z73014; AAD13922.1;
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                                                                           THR- OR GLN-RICH.
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                                                                                                                                                                                                                                                                               Oncogene 7:589-596(1992).

-!- FUNCTION: MAY CONTROL CELLULAR DIFFERENTIATION
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 3 Myb-like domains.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat.
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                                                                                                                    EMBL; Z11534; CAB37862.1; -.
HSSP; P06876; IMBG.
DictyDb; DD05044; mybA.
InterPro; IPR001005; Myb DNA_binding.
Pfam; PF00249; myb DNA-binding; 3.
SMART; SM00717; SANT; 3.
                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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16-OCT-2001
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or send an email to license@isb-sib.ch).
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ukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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MYB 2.
MYB 3.
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                                                                                                                                     DictyDb; DD02033; carC.
InterPro; IPR000848; GPCR_cAMP.
InterPro; IPR000832; GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93170666; PubMed=8382181;
Johnson R.L., Saxe C.L. III, Gollop R., Kimmel A.R., Devreotes P.N.;
"Identification and targeted gene disruption of cAR3, a cAMP receptor subtype expressed during multicellular stages of Dictyostelium
                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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28-FEB-2003
                                                                 TRANSMEM
                                                                                        Phosphorylation; Multigene
                                                                                                    PROSITE; PS50261; G_PROTEIN_RECEP_F2
G-protein_coupled_receptor; Transmem
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                                        TRANSMEM
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es Dev. 7:273-282(1993).

FUNCTION: RECEPTOR FOR CAMP. COORDINATES THE AGGREGATION
OF INDIVIDUAL CELLS INTO A MULTICELLULAR ORGANISM AND REGULATES
THE EXPRESSION OF A LARGE NUMBER OF DEVELOPMENTALLY REGULATED
GENES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS.
SUBCELLULAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: INDUCED AT EARLY AGGREGATION (6 HRS) AND
MAXIMALLY EXPRESSED AT THE MOUND STAGE (9-12HRS), LEVEL OF
PYDDERS(TON PEAKS AGAIN DURING THE SLUG STAGE (18HRS) AND DECLIN
                                                                                                                                                                                                                                                                                                                             PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED. SIMILARITY: BELONGS TO FAMILY 5 OF G-PROTEIN COUPLED RECEPTORS.
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(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                    Transmembrane; Glycoprotein;
                        EXTRACELLULAR (POTENTIAL)
                                       CYTOPLASMIC
2 (POTENTIAL
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POLY-ASN.
POLY-THR.
POLY-ASN.
 CYTOPLASMIC
                                                                            EXTRACELLULAR (POTENTIAL)
                                                              (POTENTIAL)
                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E199B3B471728F60 CRC64;
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Best Local S
Matches 16
        PIR; S52830; S52830.
TRANSPAC; T03448; --
TRANSPAC; T03500; --
SGD; S0004674; MOT3.
GO; GO:0005634; C:nucl
GO; GO:0005677; F:tran
GO; GO:0006350; P:tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
01-OCT-1996
15-SEP-2003
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MOD_RES
DOMAIN
DOMAIN
                                                                                         EMBL; U25279; AAC49982.1;
EMBL; Z48952; CAA88795.1;
PIR; S52830; S52830.
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOT3 YE,
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc finger protein MOT3/HN MOT3 OR HMS1 OR YMR070W OR
                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                              Nature 387:90-93(1997)
                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
STRAIN=S288C / AB
                                                                                                                                                                                                                                                                                                                                                                                                Madison J., Winston
Submitted (APR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                       "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                 PubMed=9169872;
      ); S0004674; MOT3.
GO:0005634; C:nucleus; IDA.
GO:0003677; F:DRA binding activity; IPI.
GO:0016564; F:transcriptional repressor
GO:0016350; P:transcription; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
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IPR007087;
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Pred. No.
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EXTRACELLULAR (POTENTIAL).
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3. 3e-07;
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                     activity; IDA
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P41151; 023615;
01-FEB-1995 (Rel. 3
16-OCT-2001 (Rel. 4
28-FEB-2003 (Rel. 4
                                                                                                                                                                         Bavan M., Bancroft I., Bent E., Love K., Goodman H.M., Dean C.,
Bergkamp R., Dirkee W., van Staveren M., Stiekema W., Drost L.,
Ridley P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,
Wedler H., Wedler E., Wambutt R., Weitzenegger T., Pohl T., Terryn N
Gielen J., Villarroel R., De Clercq R., van Montagu M., Lecharny A.,
Aubourg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,
Kotter P., Entian K.-D., Rieger M., Schaefer M., Funk B.,
Mueller-Auer S., Silvey M., James R., Monfort A., Pons A.,
Mueller-Auer S., Silvey M., James R., Monfort A., Pons A.,
Piravandi E., Obermaier B., Hilbert H., Milioni D., Hatzopoulos P.
Piravandi E., Obermaier B., Hilbert H., Benes V., Rechmann S., Ansorge W.,
Cooke R., Berger C., Delseny M., Voet M., Volckaert G., Mewes H.-W.,
Klosterman S., Schueller C., Chalwatzis N.,
Richter B., Schueller C., Chalwatzis N.,
Richter B., M., Schaefer M., Schaefer M., Mewes H.-W.,
Richter B., Schueller C., Chalwatzis N.,
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STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambut
                                                                                                                               Klosterman S., Schueller C., Chal
"Analysis of 1.9 Mb of contiguous
Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSF1 OR AT4G17750 OR DI4910C.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
Spermatophyta; Magnollophyta; eudicotyledons;
Spermatophyta; Magnollophyta; encodes; Arabidopsis.
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.

Nuclear protein; Zinc-finger; MetaI-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=99121113; PubMed=9461215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95036006;
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                                                                      SEQUENCE FROM N.A
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POLY-ASN.
POLY-ASN.
POLY-ALA.
POLY-HIS.
POLY-SER.
POLY-ASN.
POLY-ASN.
    Wambutt R.,
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C2H2-TYPE 2.
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      Murphy G.,
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         Volckaert
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RA Harris B., Ansocraw, Franct P., Grivell L.A., Rieger M., Weelchselgartner M., de Simone V., Obermaler B., Mache R., Mueller M., Ra Kreis M., Delseny M., Digdomenech P., Watson M., Schmidtheini T., Ra Reichert B., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Ra Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Wes P., Hobeisel J., Zimmermann W., Wedler H., Ridley P., Ra Langham S.-A., McCullagh B., Bilham L., Robben J., Pert R., Defoor E., Rangham S.-A., McCullagh B., Bilham L., Robben J., Pert R., Defoor E., Rangham S.-A., McCullagh B., Bilham L., Robben J., Pert R., Defoor E., Rangham S.-A., McCullagh B., Bilham L., Robbert H., Braun M., Relder B., Estates II., Aert R., Defoor E., Rangham S.-A., McCullagh B., Bilham L., Robbert H., Braun M., Robert B., Van den Daele H., Bray-Allen S., Van den Daele H., Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Ra Mocijman P., Klein Lankhorst R., Rose M., Hauff J., Koetter P., Landbert B., Van den Daele H., Peres S., Van den Daele H., Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Pereiser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., Avan Staveren M., Dirke W., Van den Daele H., Bertett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Argiriou A., Vicale D., Liguori R., Rochmann S., Argiriou A., Vicale D., Liguori R., Pirvandi E., Ra Gabel C., Puchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Bertett A., Casacuberta B., Felber R., Ra Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., Ra Gibbons T., Weber N., Schmidt W., Lecharny A., Aubourg S., Gebloi W., Johnson S., Tacon D., Jesse T., Peres R., Bertley D., Fundenbol M., Bargues M., Terol J., Torres A., Felber R., Schwiz K., Huang E., Spiegel L., Ra Stonking T., Kalikai J., Graves T., Harmon G., Edwards J., Johnson D., Marter M., Berther M., Stocker S., Gelse
                                                                                                                                          NATURE 402:769-777(1999).
NATURE 402:769-777(1999).
-!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT DROMMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
                                                                                                                                                                                                                                                                                                  thaliana.";
SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Nuclear.
PTM: EXHIBITS TEMPERATURE-DEPENDENT
                                                                                                                                      SIMILARITY)
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EMBL; X76167; CAA53761.1; -.
EMBL; 297344; CAB10555.1; -.
EMBL; AL161547; CAB78778.1;
PIR; F71447; S52641.
PINSP; P22121; 3HSF. TRANSFAC; T04394; -.
InterPro; IPR000232; HSF DNA bind.
InterPro; IPR000241; HSF ETS.
InterPro; IPR002441; HSF DNA-bind; 1.
Pfam; PF00447; HSF DNA-bind; 1.
PRINTS; PR00056; HSFDOMAIN. PD001788; HSF\_DNA\_bind; 1

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PHOSPHORYLATION

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Matches 16
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16-OCT-2001
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                                                                                                                             the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentitles requires a license agreement (See http://www.isb-sib.ch/amov send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                            Ishii N., Aoki Y., Arisawa M.;
"Molecular cloning of Rab geranylgeranyl transferase escort proteir (REP) homologue from Candida albicane.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS UNPRENYLATED RAB, PRESENTS IT TO THE CATALYTIC COMPONENT B, AND REMAINS BOUND TO IT AFTER THE GERANYLGERANYL TRANSFER REACTION. THE COMPONENT A MAY BE REGENERATED BY
                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAEP
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DOMAIN
                                                      GTPase activation. DOMAIN 419
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CANAL
                                            SEQUENCE
                                                                            PRINTS; PR00891; RABGDIREP
                                                                                      InterPro; IPR002005;
Pfam; PF00996; GDI; 1
                                                                                       Pfam;
                                                                                                          EMBL; AB021317; BAA36167.1; -.
                                                                                                                                                                                                                                                                                                                                         STRAIN=IFO 1060
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                              protein) (REP)
                                                                                                                                                                                                                                                                                                                                                                                                                                          RAB proteins
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DNA_BIND 50
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                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF
                                                                                                                                                                                                                     INHIBITOR.
                                                                                                                                                                                                                                                    TRANSFERRING ITS PRENYLATED RAB TO A PROTEIN ACCEPTOR
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; 72291 MW;
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          100.0%;
                      1.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; DNA-binding; Activator; ck; Multigene family.
 0;
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F -> Y (IN R)
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          Score 16;
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                                          POLY-ASN.
772BB6C1FF005388 CRC64;
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; 2F0DE55252B5682A CRC64;
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POLY-ASN.
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                     DB 1;
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DOMAIN
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15-JUL-1998 ()
28-FEB-2003 ()
Myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00320; GPROTEINBRPT.
PRODOM; PD000018; WD40; 2.
SMART; SM00320; WD40; 2.
PROSITE; PS00678; WD REPEATS 1; 5.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 272:11812-11815(1997).

-I- FUNCTION: PHOSPHORYLATES THREONING IN THE C-TERMINAL TAIL REGION OF MYOSIN II HEAVY CHAIN. THIS PHOSPHORYLATION IS CRITICAL IN REGULARING THE ASSEMBLY AND DISASSEMBLY OF MYOSIN II FILAMENT.

-I- CATALYTIC ACTIVITY: ATP + [myosin heavy-chain] = ADP + [myosin heavy-chain] phosphate.

-I- DOMAIN: CONSISTS OF AN N-TERMINAL DOMAIN, A CENTRAL NONREPETITIV CATALYTIC DOMAIN, AND A C-TERMINAL DOMAIN WITH SEVEN WD REPEATS.
                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHKB OR MHCKB.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004166; MHCK_EF2_kinase.
InterPro; IPR001680; WD40.
Pfam; PP02816; Alpha kinase; 1.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U90946; AAB50136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                Fransterase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC DOMAIN, AND A C-TERMINAL DOMAIN WITH SEVEN WD REPER SIMILARITY: Contains 7 WD repeats.
SIMILARITY: BELONGS TO THE MHCK / EF-2 PROTEIN KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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(Rel. 36, Last )
(Rel. 41, Last
                                                                                                732
  ilarity 100.0%; 1
Conservative 0;
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annotation update)
B (EC 2.7.1.129) (M
                      Score 16;
Pred. No.
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WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
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                                                                                                A7233C4BD56D4088 CRC64;
                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                        4.4e-07;
                                                    DB 1;
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                                               Length 732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loomis W.F.;
Submitted (AUG-1996)
-!- SIMILARITY: TO D.
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28-FEB-2003
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                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Hypothetical 85.0 kDa protein in HLJ1-
YMR164C OR YM8520.13C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=AX4;
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NCBI_TaxID=44689;
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Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                  YM38 YEAST
Q03825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                   SEQUENCE FROM N.A.
STRAIN=S288c / ABS
PubMed=9169872;
                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DictyDb; DD01058; cigB.
InterPro; IPR000315; Znf
Pfam; PF00643; zf-B_box;
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(Rel. 41, Last annotation update)
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HLJ1-SMP2 in
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                                  Saren A.M., Laamanen P., Lejarcegui J.B., Paulin L.;
"The sequence of a 36.7 kb segment on the left arm of chromosome IV
"From Saccharomyces cerevisiae reveals 20 non-overlapping open reading
frames (ORFs) including SIT4, FAD1, NAM1, RNA11, SIR2,NAT1,PRP9, ACT2
and MPS1 and 11 new ORFs.";
Yeast 13:65-71(1997).
                                                                                                                                                                                     MEDLINE=98190081; PubMed=9524122;
Xue Y., Batlle M., Hirsch J.P.;
"GPR1 encodes a putative G protein-coupled receptor that associates
with the Gpa2p Galpha subunit and functions in a Ras-independent
                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Q12361;
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                                                                                                                          SEQUENCE FROM
STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                              MEDLINE=97197972; PubMed=9046088;
                                                                                                                                                                 EMBO J.
                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                protein-coupled R1 OR YDL035C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0004774; MSS11.
GO:0005034; C:nucleus; IC.
GO:0005704; F:specific RNA polymerase II transcription fa...
GO:00045044; P:positive regulation of transcription from P...
GO:0007124; P:pseudohyphal growth; IGI.
GO:0005983; P:starch catabolism; IMP.
FUNCTION: Seems to associate coupled receptor that senses growth. It acts upstream of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S54522; S54522.
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16; Conservative (
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51 8;
290 32
605 63
653 65
758 AA; 1
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sociate with GPA2 and act
senses glucose and contr
eam of adenylate cyclase
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POLY GLN.
POLY-ASN.
POLY-SER.
POLY-SER.
W; BA05BFC754D9294B CRC64;
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Pred. No.
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RESULT 15
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EMBL; Z71781; CAA98454.1; -.
PIR; S67568, S67568
SGD; S0002193; GPR1.
GG; GO:0005886; C:plasma membrane; IDA.
GG; GO:0004930; F:G-protein coupled receptor gG; GO:0007126; P:G-protein coupled receptor IRO; GO; GO:0007124; P:pseudohyphal growth; IMP.
GG; GO:0007124; P:pseudohyphal growth; IMP.
GG; GO:0007124; P:pseudohyphal growth; IMP.
GG; GO:0007124; P:pseudohyphal growth; IMP.
GG; GO:0007124; P:pseudohyphal growth; IMP.
GG; GO:0007124; P:pseudohyphal growth; IMP.
GG; GO:0007124; P:pseudohyphal growth; IMP.
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TRANSMEM 134 156
TRANSMEM 179 198 POTENTIAL.
TRANSMEM 179 198 POTENTIAL.
TRANSMEM 251 273 POTENTIAL.
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01-FEB-1995
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15-SEP-2003
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or send a
                                                                                               PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX."
Nature 387.84-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                    01-FEB 1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Putative 108.8 kDa transcriptional regulato
                                                                                                                                                                                                                         STRAIN=S288c
                                                                                                                                                                                                                                     SEQUENCE FROM N.
                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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                                                                        SIMILARITY:
                                                                                    SUBCELLULAR
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                                                                     LOCATION: Nuclear (Probable).
Contains 1 Zn(2)-Cys(6) fungal-type
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PTP3 DICDI
DTP3 DICDI
STANDARD; PRT; 989 AA.
AC P54637;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 35, Last annotation update)
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PROSITE; PS50048; ZN2_CY6_FUNGAL_2;
Hypothetical protein; Transcription;
Nuclear protein; Zinc; Metal-binding
DNA_BIND 21 47 ZN(2)-C;
DOMAIN 811 896 ASN-RICE
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Pfam; PF04082; Fungal trans;
Pfam; PF00172; Zn_clus; 1.
SMART; SM00066; GAL4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96189126; PubMed=8628311; Gamper M., Howard P.K., Hunter T., Firtel R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Matches 16
                                                                                                                                                                                                                                                                                                                                     "SUZ2_DRUMD
P25172;
01-MAY-1992 (Rel. 22
01-MAY-1992 (Rel. 22
16-OCT-2001 (Rel. 4
EMBL;
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PIR; S
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00102; Y_phosphatase;
PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                               Suppressor 2 SU(Z)2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                               Nucleic Acids Res. 19:3149-3149(1991).
-!- FUNCTION: REGULATES EXPRESSION OF THE HOMEOTIC SELECTOR GENES BY INFLUENCING HIGHER-ORDER CHROMATIN STRUCTURE THROUGH INTERACTION
                                                                                                                                                                                                                    MEDLINE=91279476; PubMed=2057369; Brunk B.P., Adler P.N.;
                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                           STRAIN=Canton-S
                                                                                                                                                                                                                                                                        Ephydroidea; Drc
NCBI_TaxID=7227;
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                                                                                                                             SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Contains 1 RING-type zinc finger.
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S; PR00700; PK11...
I; SM00194; PTPC; 1.
ITE; PS00383; TYR_PHOSPHATASE_1; 1.
                                                                                                                                                    FUNCTION: REGULATES EXPRIINFLUENCING HIGHER-ORDER WITH OTHER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           742
 S14871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       137
          X56798; CAA40134.1; -. X56799; CAA40135.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989
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llarity 100.0%;
Conservative (
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460
109
137
249
258
258
286
366
787
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983
943
                                                                                                                                                                                                                                                                                      Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                    Z.A
                                                                                                                                                                                                         of the Drosophila regulatory gene Suppressor
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1. 22,
1. 40,
zeste
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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190
257
265
289
289
371
790
839
892
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Last annotation update)
protein (Protein posterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                       152
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POLY-ASN.
POLY-ASN.
POLY-ASN.
POLY-SER.
POLY-SER.
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POLY-ASN.
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Pred. No. 5.8e-07;
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1; 9371105AF80974AF CRC64;
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Usage

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outstation

use by non-profit institutions as long a modified and this statement is not removed.

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RESULT 18
KYK1_DICDI
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Query Match
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Matches 16
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InterPro; IPR001841; Znf ring.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc-finger;
ZN_FING
DOMAIN 6
DOMAIN 10
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P18160;
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Nuckolls G.H., Osherov N., Loomis W.F.,
"The Dictyostelium dual-specificity kins
spore-differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16,
01-OCT-1996 (Rel. 34,
28-FEB-2003 (Rel. 41,
                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                          Dictyostelium discoideum.",
Mol. Cell. Biol. 10:3578-3583 (1990).
-i- FUNCTION: ESSENTIAL FOR SPORE DIFFERENTIATION.
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90287147; PubMed=1972546;
Tan J.L., Spudich J.A.;
"Developmentally regulated protein-tyrosine kinase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase 1).
PYKA OR SPLA OR DPYK1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1248-1584 FROM N.A.
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                                                                                                                                                                                tyrosine phosphate.

DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITDEVELOPMENT STAGE OF MORPHOGENESIS.

SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.

SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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Last annotation updat
kinase spore lysis A
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POLY-ASN.
POLY-SER.
MISSING (IN REF. 1
A -> R (IN REF. 1
MISSING (IN REF. 1
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spore lysis A (EC
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Pred. No.
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D -> E (IN REF. 1; CAA40134

MISSING (IN REF. 1; CAA40134

A -> P (IN REF. 1; CAA40134

MW; 7B4BA0F35B0FA683 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase splA is essential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; L, 7.9e-07;
                                                                                                                                                                                                                                                                                              tyrosine = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spudich J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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1; CAA40134).
F. 1; CAA40134).
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ADP

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RESULT 19
P3K3_DICDI
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Best Local S
Matches 16
                                                                                                                                                              P3K3_ICDI STANDARD; PRT; 15:
P54675;
01-OCT-1996 (Rel. 34, Last sequence up:
01-OCT-1996 (Rel. 34, Last annotation:
16-OCT-2001 (Rel. 40, Last annotation:
Phosphatidylinositol: 3-kinase: 3 (EC 2.)
(PtdIns-3-kinase) (PIJK) (Fragment).
PIKC OR PIK3.
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DOMAIN 9
DOMAIN 4
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BINDING
ACT SITE
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DOMAIN
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DOMAIN
DOMAIN
MEDLINE=96009592; PubMed=7565716; Zhou K., Takegawa K., Emr S.D., Firtel R.A.; Takegawa K., Emr S.D., Firtel Really in Dictyostelium "A phosphatidylinositol (PI) kinsee family in Dictyostelium discoideum: biological roles of putative mammalian p110 and yeast Vps34p PI 3-kinase homologs during growth and development."; Mol. Cell. Biol. 15:5645-5656(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00454; SAM; 1.
SMART; SM00449; SPRY; 3.
PROSITE; PS00107; PROTEIN KINASE ATP;
PROSITE; PS50011; PROTEIN KINASE DOM;
PROSITE; PS00109; PROTEIN KINASE TYR;
PROSITE; PS50105; SAM_DOMĀIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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ProDom; PD000001; Prot_kinase;
                                                                                   STRAIN=AX3;
                                                                                              SEQUENCE
                                                                                                                       NCBI_TaxID=44689;
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InterPro; IPR003877;
InterPro; IPR001245;
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DictyDb; DD03010;
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InterPro; IPR000719; Pr
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PF00536; SAM; 1.
PF00622; SPRY; 3.
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M33785; AAA33202.1;
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16; Conserv
                                                                                              FROM N.A.
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
linositol 3-kinase 3 (EC 2.7.1.137)
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Tyr_pkinase.
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POLY-GLN.
POLY-GLN.
POLY-PRO.
POLY-PRO.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
D -> R (IN REF. 2).
V -> L (IN REF. 2).
V -> L (IN REF. 2).
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Pred. No.
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POLY-ASN.
POLY-ASN.
POLY-ASN.
POLY-ASN.
POLY-ASN.
POLY-PHE.
POLY-SER.

    kinase; ATP-binding; Phosphorylation.

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InterPro; IPR000403; PI3 PI4 kinase.
InterPro; IPR002420; PI3K C2.
InterPro; IPR002420; PI3K C3.
InterPro; IPR001263; PI3Ka.
Pfam; PF00454; PI3 PI4 kinase; 1.
Pfam; PF00792; PI3K C2; 1.
Pfam; PF00794; PI3K rbd; 1.
Pfam; PF00794; PI3K rbd; 1.
SMART; SM00142; PI3K C2; 1.
SMART; SM00144; PI3K C2; 1.
SMART; SM00144; PI3K C3; 1.
SMART; SM00145; PI3KG; 1.
SMART; SM00145; PI3KG; 1.
SMART; SM00146; PI3KG; 1.
                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Prestalk-specific protein tagC precursor (EC TAGC.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00915; PI3_4 KINASE_1; 1.
PROSITE; PS00916; PI3_4 KINASE_2; 1.
PROSITE; PS50290; PI3_4 KINASE_3; 1.
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-!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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-!- FUNCTION: INTERCELLULAR COMMUNICATION VIA TAGC MAY MEDIATE INTEGRATION OF CELLULAR DIFFERENTIATION WITH MORPHOGENESIS SIMILARITY).
-!- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO PEPTIDASE S8.
-!- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE ATP-E-SIMILARITY: IN THE C-TERMINAL SECTION.
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Shaulsky G., Escalante R., Loomis W.F.;
"Developmental signal transduction path
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SMART; SM00382; AAA; 1.

PROSITE; PS00211; ABC TRANSPORTER 1; 1.

PROSITE; PS00136; SUBTILASE ASP; FALSE NEG.

PROSITE; PS00137; SUBTILASE HIS; 1.

PROSITE; PS00138; SUBTILASE SER; FALSE NEG.
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Pfam; PF00723; SUBTILISIN.
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Interpro; IPR000341; p13K C2:
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Interpro; IPR000341; p13K ras bind.
Interpro; IPR001263; p13Ka;
Pfam; PF00454; P13 P14 kinase; 1.
Pfam; PF00792; P13K C2; 1.
Pfam; PF00792; P13K C2; 1.
SMART; SM00142; P13K rbd; 1.
SMART; SM00142; P13K rbd; 1.
SMART; SM00145; P13K rbd; 1.
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PROSITE; PS00915; P13 4 KINASE 1; 1.
PROSITE; PS00915; P13 4 KINASE 2; 1.
PROSITE; PS00916; P13 4 KINASE 3; 1.
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Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
"A phosphatidylinositol (PI) kinase gene family in Dictyostelium
"A phosphatidylinositol (PI) kinase gene family in Dictyostelium
discoideum: biological roles of putative mammalian pl10 and yeast
Vps34p PI 3-kinase homologs during growth and development.";
Mol. Cell. Biol. 15:5645-5656(1995)
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = AL
1-phosphatidyl-1D-myo-inositol 3-phosphate.
-!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Phosphatidylinositol 3-kinase 2 (EC 2.7.1.137)
(PtdIns-3-kinase) (PI3K).
                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                    MEDLINE=95262903; PubMed=7744252; Shaulsky G., Kuspa A., Loomis W.F.; Shaulsky G., Kuspa A., Loomis W.F.; Shaulsky G., Kuspa A., Loomis W.F.; Gries protease gene is received for prestalk specialization in Dictyostelium."; Genes Dev. 9:111-1122(1995).
-i- FUNCTION: INTERCELLULAR COMMUNICATION WITH MORPHOGENESIS: INTEGRATION OF CELLULAR DIFFERENTIATION WITH MORPHOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                     TAGB_DICDI STANDARD; PRT; 1905 AA. P54683; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Prestalk-specific protein tagB precursor (EC
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SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
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PRODOM; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00121; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.
PROSITE; PS00137; SUBTILASE_SER; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
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01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Clustered-asparagine-rich protein (Fra
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Hae
NCBI\_TaxID=5833;

Apicomplexa; Haemosporida;

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RC STRAIN=5288c / AB972;

RC STRAIN=5288c / AB972;

RX MEDLINE=97313271; PubMed=9169875;

RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,

RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

RA Araujo R., Dearicio A., Barrell B.G., Badcock K., Benes V.,

RA Churg E., Churcher C.M., Coster F., Davis K., Davis R.W.,

RA Churg E., Churcher C.M., Coster F., Davis E., Duesterhoeft A.,

RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

RA Hall J., Hebling U., Heumann K., Hilbert H., Hiller L.,

RA Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

RA Komp C., Kurdi O., Lashkari D., Lew H., Mirtipati S., Moestl D.,
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MEDLINE=86206015; PubMed=3517875;
Wahlgren M., Aaslund L., Franzen L.,
Wahlgren K., McNicol L.A., Bjoerkman
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Q08925;
30-MAY-2000
30-MAY-2000
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Pfam; PF00076; rrm; 2
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-!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
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01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucose-repressible alcohol dehydrogenase transcriptional effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformathe European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                  MEDLINE=93093455; PubMe Malvar T., Biron R.W.,
                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclascharomycetales; Saccharomycetaceae; Saccharomyces
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-!- SIMILARITY: TO S.POMBE SPCC737.01C AND
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                                                            "The CCR4 protein from leucine-rich repeat req
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"Molecular cloning of chromosome I DNA from Saccharomyces cerevisiae:
analysis of the genes in the FUN38-MAK16-SPO7 region.";
J. Bacteriol. 176:1872-1880(1994).
-i- FUNCTION: CONTROL OF ADH2 GENE EXPRESSION. IT IS REQUIRED FOR THE
-i- FUNCTION: CONTROL OF ADH2 GENE EXPRESSION. IT IS REQUIRED FOR THE
EXPRESSION OF GENES INVOLVED IN NONFERMENTATIVE GROWTH AND IT
MEDIATES OR IS REQUIRED FOR THE ACTION OF THE SPT6 & SPT10 GENES.
-i- MISCELLANEOUS: THE 169 CARBOXYL-TERMINAL RESIDUES ARE IMPORTANT
                                                                                                                                                                                                                                                                                                                                                        riam; PF03372; Exo_endo_phos; Pf4am; PF00560; LRR; 3. PRINTS; PR00019.
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
P25339;
01-MAY-1992 (Rel.
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                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00019; LEURICHRPT SMART; SM00369; LRR_TYP; 1.
                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                         Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T03228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zeng B., Fortin
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                            ; S0000019; CCR4.
; S0000019; CCCR4-NOT core complex; IPI.
GO:0030015; C:CCR4-NOT core complex; IPI.
GO:0005737; C:cytoplasm; IDA.
GO:0000175; F:3'-5' exoribonuclease activity; IDA.
GO:0000289; P:poly(A) tail shortening; IDA.
GO:0006357; P:regulation of transcription from Pol II pro. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains
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                                                                                                             742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S50459; AAB24455.1;
L05146; AAC04936.1;
                                                                                      89
                                                                                                                                   l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                   NNNNNNNNNNNN 756
                                                                                      NNNNNNNNNNNN 103
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IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.F.F., Clark M.W., Keng T., Storms R.K., Zhong W.W., Fortin N., Delaney S., Barton A.B., Kaback D.B., Bussey H., ng of chromosome I from Saccharomyces cerevisiae: analysis b region between the LTB1 and SPO7 genes.";
                                                                                                                                                                                                                                       15
190
190
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403
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                     regulation;
                                                                                                                                                                                      ΑA;
                        STANDARD;
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22, Created)
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POLY-GLN.
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L ->
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VI)
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4.7e-06;
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EMBL; S58126; AAD13898.1; -.
EMBL; Z72536; CAA96714.1; -.
PIR; 'S64016; S64016.
SGD; S0002982; PUF4.
GO; GO:00007569; P:ccell aging; IGI.
GO; GO:0000288; P:mRNA catabolism, dead
GO; GO:0006605; P:protein targeting; IM
InterPro; IPR001313; Pumilio/Puf.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91353083; PubMed=1882553; Choder M., Goffeau A.; Chen W., Balzi E., Capleaux E., Choder M., Goffeau A.; "The DNA sequencing of the 17 kb HindIII fragment spanning the and ATE1 loci on chromosome VII from Saccharomyces cerevisiae r the PDR6 gene, a new member of the genetic network controlling pleiotropic drug resistance."; Yeast 7:287-299(1991).
                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hebling U., Hofmann Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                  REFEAT
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Metal-binding;
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-!- SIMILARITY: SOME, TO YEAST YJR091C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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YGL014W OR YGL023.
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ling U., Hofmann B., Delius H.;
mitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
FUNCTION: Is not essential for haploid growth, but I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diploid formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced een the Swiss Institute of Bioinformatics and
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                                                                                                                                                                                                                                                  PF00806; PUF;
   Similarity
15; Conser
                                                                                                                                                                                                                                     SM00025; Pumilio;
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   Conservative
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100.0%; --
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                            1.2%;
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  Score 15; DB; Pred. No. 5e-
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ASN-RICH.
POLY-ASN (POTENTIAL ACTIVATING DOMAIN).
C4-TYPE.
                                                  -> R (IN REF. 1 AND 2).
659BA1062439F642 CRC64;
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PDR6-PDR1
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                          Length 888;
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-phosphatidylinositol-3-phosphate 5-kinase F;
(Phosphatidylinositol-3-phosphate 5-kinase) (?
FABI OR YFR019W.
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P34756;
              modified
entities
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                                                                                                                                                                                                                                          Waldmann T., Lupas A., Kellermann J., Peters J., Baumeister W.;
"Primary structure of the thermosome from Thermoplasma acidophilum.";
Biol. Chem. Hoppe-Seyler 376:119-126(1995).

-i- FUNCTION: Catalyzes the phosphorylation of phosphatidylinositol-3-
phosphate on the fifth hydroxyl of the myo-inositol ring, to form
phosphatidylinositol-4,5-biphosphate. Required for endocytic-
vacuolar pathway and nuclear migration. The product of the
reaction it catalyzes functions as an important regulator of
vacuole homeostasis perhaps by controlling membrane flux to and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95400292; PubMed=7670463;
Murakami Y., Naitou M., Hagiwara
Sasanuma S.-I., Sasanuma M., Tsuc
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                                                                                          This
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The stress-activated phosphatidylinositol 3-phosphate 5-kinase is essential for vacuole function in S. cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cooke F.T., Dove S.K., McEwen R.K., Hall M.N., Michell R.H., Parker P.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cooke F.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99035548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=95392039;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Curr. Biol. 8:1219-1222(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Novel PI(4)P 5-kinase homologue,
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                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95314774; PubMed=7794526;
                                                                                                                  COPACTOR: Magnesium or Manganese.
SUBCELLULAR LOCATION: VACUOLE-ASSOCIATED (POTENTIAL).
SIMILARITY: BELONGS TO THE PTDINS(4)P-5-KINASE FAMILY.
SIMILARITY: Contains 1 FYVE-type zinc finger.
                                                           European Bioinformatics Institute.
                                                                                                                                                                                      bisphosphate.
                                                                                                                                                                                                 monophosphate = ADP
                                                                                                                                                                                                                   CATALYTIC ACTIVITY:
                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                   from the vacuole.
              and this statement is not removed. Usage by requires a license agreement (See http://www.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and morphology in yeast.";
L. Cell 6:525-539(1995).
                                             non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2039; PubMed=7663021;
Dewald D.B., Boronen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB972;
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shiro H., Eki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9811604;
                                                                                                                                                                                                   ATP + 1-phosphatidyl-1D-myo-inositol + 1-phosphatidyl-1D-myo-inositol 4,5-
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a Y., Soeda
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E., Yokoyama
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: III PIP kinase).
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(See http://www.isb-sib.ch/announce/

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RESULT 28
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                                                                                                                                    assembly in Xenopus laevis egg extracts.";
J. Cell Biol. 136:859-870(1997).
J. Cell Biol. 136:859-870(1997).
II. FUNCTION: PROMOTES MITOTIC SPINDLE ASSEMBLY.
II. DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS; A SOLUTION CONTRAL ALPHA-HELICAL COILED COIL M. TERMINAL, A CENTRAL WHICH IS RESPONSIBLE FOR THE GLOBULAR C-TERMINAL WHICH IS RESPONSIBLE FOR THE (IT HYDROLYZES ATP AND BINDS MICROTUBULES).
II. SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN E
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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15-JUL-1998 (Rel. 36, Las
16-OCT-2001 (Rel. 40, Las
Carboxy-terminal kinesin
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ZN FING 240 2
DOMAIN 393 3
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SGD; S0001915; FAB1.
                                                                                                                                                                                                                                                                         Walczak C.E., Verma S., Mitchison T.J.;
"XCTK2: a kinesin-related protein that promotes mitotic
                                                                                                                                                                                                                                                                                                                                TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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InterPro; IPR000306;
                                                                                                                                                                                                                                                                                                             MEDLINE=97201465; PubMed=9049251;
                                                                                                                                                                                                                                                                                                                                                                                                              Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0000285; F:1-phosphatidylinositol-3-phosphate 5-kinase.
GO:0006644; P:phospholipid metabolism; IGI.
GO:0007033; P:vacuole organization and biogenesis; IMP.
                                                   European Bioinformatics Institute.
                                                                                                                        SUBFAMILY.
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                                                                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards G., Chang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Boothakov S.,
RA Borkova D., Botchan M.R., Bouck J., Barokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Barokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kunlo D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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P20480; Q9VAGB;

01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Drotein.
NCD OR CA(ND) OR CG7831.
NCD OR CA(ND) OR CG7831.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insect.
Neoptera; Endopterygota; Diptera; Brachycera; Mu
Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE
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MEDLINE=20196006; PubMed=10731132;
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PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1
Motor protein; Microtubules; ATF-binding;
DOMAIN 1 116
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Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng S.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith i Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) (
MEDLINE=96.195067; PubMed=8606780;
Sablin E.P., Kull F.J., Cooke R., Vale
"Crystal structure of the motor domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moore J.D., Song H., Endow S.A.; "A point mutation in the microtubule protein reduces motor velocity.";
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Komma D.J., Horne A.S., Endow S.A.;
Komma D.J., Horne A.S., Endow S.A.;
"Separation of meiotic and mitotic effects of
non-disjunctional on chromosome segregation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91043032; PubMed=2146510; Walker R.A., Salmon E.D., Endow S.A.; "The Drosophila claret segregation pr
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-!- FUNCTION: NCD IS REQ
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MEDLINE=91122049; Pu
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- SIMILARITY: BEL
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arfan D., Frise E., George
G., Miranda A., Mungall C.
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SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor_protein; Cell_division; Microtubules;
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GO; GO:0007100; P:centrosome separation; IGI.
GO; GO:0000212; P:meiotic spindle assembly; NAS.
InterPro; IPR001752; kinesin motor.
Pfam; PF00225; kinesin; 1.
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EMBL; M33932; AAA28716.1; --
EMBL; AE003771; AAP56942.1; --
EMBL; AY058596; AAL13825.1; --
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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-!- FUNCTION: REGULA:
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                            TISSUE=Ovary;
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           mitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. FUNCTION: REGULATES MICROTUBULE DYNAMICS DURING MITOTIC SE ASSEMBLY. REQUIRED FOR BOTH ESTABLISHMENT AND MAINTENANCE MITOTIC SPINDLES. MAY ACT DIRECTLY ON MICROTUBULES, CAUSIN DESTABILIZATION AND EVENTUAL DEPOLYMERIZATION OF THE MICRO
SUBUNIT: Homodimer
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                  Mayer K.F.X., Schweller C., Wambutt R., Murphy G., Volckaert G.
pohl T., Duesterhoeft A., Sriekema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mecher B., Mache R., Muell
Weichselgartner M., de Simone V., Obermaier B., Mache R., Muell
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini
Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancrof
Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
Vandenbussche
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P46864; Q9T047;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upda:
15-SEP-2003 (Rel. 42, Last annotation up
Kinesin 2 (Kinesin-like protein B).
ATK2 OR KATB OR AT4027180 OR T24A18.130.
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PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
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                                                                                                                                                                                                               STRAIN=cv. Columbia; MEDLINE=9435659; PubMed=8075402; MEDLINE=9435659; PubMed=8075402; Mitsui H., Nakatani K., Yamaguchi-Shinozaki K., Nishikawa K., Takahashi H.; "Sequencing and characterization of the kinesinand katC of Arabidopsis thaliana."; Plant Mol. Biol. 25:865-876(1994).
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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HSSP; P17119; 3KAR.
InterPro; IPR001752; kinesin_motor.
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RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Ram Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., RA De Keyser A., Rogers J., Cronin A., Quail M., Bray-Allen S., RAY M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Dose S., de Haan M., Marse A.C., Schaefer M., Mclehnert T.-H., RA Dose S., de Haan M., Vitale D., Liguori R., Piravandi E., RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., RA Chiabbi S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Cheidor F., Cooke R., Berger C., Monfort A., Casacuberta E., Cordee R., Berger C., Monfort A., Casacuberta E., Corde R., Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., RA Heijnen L., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Perrell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Fishman D., Haase D., Lencke K., Mewes H.-W., Stocker S., Shele P., Cordes M., Abu-Threideh J., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Parnell L., Berghoff A., Jones K., Drone K., Cotton M., Joshu C., RA Autoniu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., RA Parnell L., Schutz M., Habergawa A., Hameed A., Lodhi M., Johnso
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL035680; CAB38848.1; ALT_SEC
EMBL; AL161566; CAB79573.1; ALT_SEC
PIR; T06048; T06048.
HSSP; P17119; 3KAR.
InterPro; IPR001752; kinesin_motor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce
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- PUNCTION: POSSIBLE OF THREE STRUCTURAL DOMAINS; A SMALL COMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS; A SMALL COMPOSED OF THREE STRUCTURAL COILED COIL AND A INTERMINAL, A CENTRAL ALPHA-HELICAL COILED FOR THE MOTOR GLOBULAR C-TERMINAL WHICH IS RESPONSIBLE FOR THE MOTOR (IT HYDROLYZES ATP AND BINDS MICROTUBULES).

-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                   Motor protein; Microtubules;
                                                                                                                                                                                                                                                                     PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00225; kinesin;
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                                                                                                                                                                                                                                                                                                                                                         SM00129; KISC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
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479
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COILED COIL.
KINESIN-MOTOR (BY SIMILARITY)
ATP (POTENTIAL).
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DOMAIN
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                                                          PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
PROSITE; P800411; KINESIN MOTOR DOMAIN1;
PROSITE; P850067; KINESIN_MOTOR_DOMAIN2;
                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced th between the Swiss Institute of Bioinformatics and t the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO T
SUBFAMILY.
-!- CAUTION: Ref.2 sequence
gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequencing and characterization of and katC of Arabidopsis thaliana."; Plant Mol. Biol. 25:865-876(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinesin 3 (Kinesin-like protein C).
ATK3 OR KATC OR AT5G54670 OR K5F14.1 OR
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARATH
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-!- FUNCTION: POSSIBLE ROLE IN MITOSIS.
                                                                                                                                                   Pfam; PF00225; kinesin;
                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                    EMBL; AB022214;
                                                                                                                                                                                                                                                             EMBL; D21138; BAA04674.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural analysis of features of the regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitsui H., Nakatani K., Yamaguchi-Shinozaki
Nishikawa K., Takahashi H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbia;
MEDLINE=94355659; PubMed=8075402;
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                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS; A SMALL GLOBULAR N-TERMINAL, A CENTRAL ALPHA-HELICAL COILED COIL AND A LARGE GLOBULAR C-TERMINAL WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY (IT HYDROLYZES ATP AND BINDS MICROTUBULES).

SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. NCD
                                                                                                                                                                                                                  S48020; S48020.
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                                        protein; Microtubules;
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                                                                                                                                                                IPR001752; kinesin_motor
                  family.
                                                                                                                                                                                                                                                                                                        email to license@isb-sib.ch).
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                                                                                                                                                                                                                                         BAB09933.1;
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Y., Kaneko T., K
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4e-05;
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                                           coil;
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RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Langham S.-A., Wcltipens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Liankhorst R., Rose M., Hauf J., Koetter P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Pelber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Pelber R.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Prishman D., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
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ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of a gene family (k in Arabidopsis thaliana and the chastructure of Kath.";
Mol. Gen. Genet. 238:362-368(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=20083488; PubMed=10617198;
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ATK1 OR KATA OR AT4G21270 OR F7J7.210.
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15-SEP-2003 (Rel.
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KINESIN-MOTOR (BY SIMILARITY).
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Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.
Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
Melson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shahh R.,
Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
Chen E., Marra M., Martienssen R., McComble W.R.;
                                                                                                        DOMAIN
NP BIÑD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Development 129:2401-2409(2002).

-i- FUNCTION: Kinesin that supports microtubule movement in an dependent manner and has a minus-end directed polarity. Pl. crucial role in spindle morphogenesis in male Arabidopsis in ATK1 mutants, male meiosis is defective, producing an al number of microspores of variable sizes.

-i- DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS; A SMALL GLOBING-TERMINAL, A CENTRAL ALPHA-HELICAL COLLED COIL AND A LARGI GLOBULAR C-TERMINAL WHICH IS RESPONSIBLE FOR THE MOTOR ACTION OF THE MICROTURBULES).

-i- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. NCI
                                                                                                                                                                                                                                         Motor prot
Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12112142;

PubMed=12112142;

Marcus A.I., Ambrose J.C., Blickley L., Hancock W.O., Cyr R.J.;

Marcus A.I., Ambrose J.C., Blickley L., Hancock W.O., Cyr R.J.;

"Arabidopsis thaliana protein, ATKI, is a minus-end directed kinesin that exhibits non-processive movement.";

that exhibits non-processive movement.";

Cell Motil. Cytoskeleton 52:144-150(2002).
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Chen C., Marcus A.,
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                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISC; 1.
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RI Nature 415:871-880(2002).

"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002).

"The genome sequence of Schizosaccharomyces pombe.";
C. -! SUBCELLULAR LOCATION: Nuclear.

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C. -! SUBCELLULAR E.CCATION: Nuclear.
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Q92376; O42669;
01-NOV-1997 (Re
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                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewar
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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15-DEC-1998 (Rel. 37, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97053988; PubMed=8898367;
Pidoux A.L., Ledizet M., Cande W.Z.;
"Fission yeast pkl1 is a kinesin-related protein involved in mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinesin-like protein
PKL1 OR SPAC3A11.14C
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                                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY.
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                                                                                                              an email to license@isb-sib.ch).
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Benito J.,
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RESULT 35
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Q03101;
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                                                                         MEDLINE=98054247; PubMed=9391039;
Liu Y., Ruoho A.E., Rao V.D., Hurley J.H.
"Catalytic mechanism of the adenylyl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1
PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1
Motor protein; Microtubules; ATP-binding;
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                                                                                                                                                                                                                              different roles in Dic
Cell 69:305-315(1992).
                                                                                                                                                                                                                                                            Pitt G.S., Milc Devreotes P.N.;
                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                    -!- SIMILARITY: Contains 1 CHASE domain.
                                                                                                                                                                                                                                       "Structurally distinct and stage-specific adenylyl cyclase different roles in Dictyostelium development.";
                                                                                                                                                                                                                                                                               MEDLINE=92233467;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                             Adenylate cyclase,
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                                                                                                                                                                                                           D-STRUCTURE MODELING OF 387-543.
                                               SIMILARITY: Belongs to cyclase family.
                                                                 DURING GERMINATION.
        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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284
344
482
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343
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(Rel. 26, Last sequence update)
(Rel. 41, Last annotation update)
yClase, germination specific (EC 4)
te-lyase) (Adenylyl cyclase).
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N., Borleis J.,
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P46865;
01-NOV-1995
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Pfam; PF00211; guanylate_cyc;
SMART; SM00044; CYCc; 1.
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                                                                        SEQUENCE FROM N.A.
STRAIN=MHOM/BR/82 / Isolate BA-2;
MEDLINE=93133867; PubMed=8421715;
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                                                                                                                                                                              Leishmania chagasi.
Eukaryota; Euglenozoa;
NCBI_TaxID=44271;
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InterPro; IPR001054; G_cyclase.
"Molecular characterization of a kinesin-related antigen
                                                                                                                                                                                                                                                                                 Kinesin-like
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(Rel. 34,
protein K
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                                                Shreffler W.G.,
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                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
K39 (Fragment).
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k; Pred. No. 4.5
0; Mismatches
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                                                   Benson
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                                                D.R.,
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OR (TYPE-II MEMBRANE PROTEIN)
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                                                Ghalib H.W.,
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P43565;
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PIR; A47334; A47334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Serine/threonine-protein kinase RIM15 (EC 2
RIM15 OR TAKI OR YFL033C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

PS50067; KINESIN MOTOR DOMAIN2; 1.

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PS60067; KINESIN MOTOR DOMAIN2; 1.

PS60067; KINESIN MOTOR DOMAIN1; 1.

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PS60067; KINESIN MOTOR DOMAIN2
                            [2]
SEQUENCE FROM N.A.,
                                                                                                                 MEDLINE=95400292; PubMed=7670463; Murakami Y., Naitou M., Hagiwara Sasanuma M., Tsuc Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide seque Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Bake
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
28-FEB-2003 (Rel. 41,
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SMART; SM00129; KISC;
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Proc. Natl. Acad. Sci. U.S.A. 90:775-779(1993).
-i- DEVELOPMENTAL STAGE: PREDOMINANT IN AWASTIGOTES.
-i- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
MEDLINE=97265402;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seishmania chagasi that detects
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae (Baker's yeast).
ngi; Ascomycota; Saccharomycotina; Saccharomycetes;
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   PubMed=9111339;
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                            AND CHARACTERIZATION
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a Y., Soeda
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5e-05;
                                                                                                                                                       chromosome
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                                                                                                                                                                                                             Ozawa M.,
E., Yokoyama
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Matches 14
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ACT_SITE
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                                                                                                                                                                                                                                                                                                   SMART; SM00448; REC; 1.

SMART; SM00133; S_TK X; 1.

SMART; SM00220; S_TKG; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; F
PROSITE; PS00101; PROTEIN_KINASE_BOM; 1
PROSITE; PS00100; PROTEIN_KINASE_ST; 1.

PROSITE; PS00100; RESPONSE_REGULATORY;
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase; 1.
Pfam; PF00072; response reg; 1.
ProDom; PD000001; Prot kinase; 2
ProDom; PD000039; Response_reg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0006466; P:protein amino acid phosphorylation; GO; GO:0040020; P:regulation of meiosis; IMP. GO; GO:0006950; P:response to stress; IMP. InterPro; IPR000961; Pkinase_C. InterPro; IPR000719; Prot kinase_C. InterPro; IPR001789; Response reg. InterPro; IPR001789; Response reg. InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reinders A., Buerckert N., Boller T., Wiemken A., de Virgilio C.; "Saccharomyes cerevisiae cAMP-dependent protein kinase controls en into stationary phase through the Rimisp protein kinase."; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE ACTIVATION OF A MEIOTIC GENES ACTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Stimulation of yeast meiotic gene expression glucose-repressible protein kinase Rim15p."; Mol. Cell. Biol. 17:2688-2697(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D50617; BAA09206.1; -. EMBL; U83459; AAB64088.1; -.
                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                      Transferase; Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 response regulatory domain.
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SIMILARITY: BELONGS TO THE
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S0001861; RIM15.
345
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                                                      14;
                                                                     Similarity
NNNNNNNNNNNN
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1636
343
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POLY-ASN.
POLY-SER.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-ASN.
POLY-GLU.
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Pred. No.
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Bioinformatics and the EMBL outstation -
                                                         Mismatches
                                                                                                             DC1064825000FAFF
                                                                                                                                                                                                                                                                                       kinase;
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                                                                   DB 1; L
. 8.9e-05;
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                                                                               Length 1770;
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                                                                                                             CRC64;
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RESULT 38
YM8D\_YEAST

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RESULT 39
HKLB_LYCES
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Best Local
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P38429; Q03501;
01-OCT-1994 (Rel. 3
01-NOV-1997 (Rel. 3
                                                                           15-JUL-1999
15-JUL-1999
28-FEB-2003
                                                                                                            HKLB LY(
022300;
                                                                                                                                                                                                                                                                                     CONFLICT
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SGD; S0004876; SAP30.
GO; GO:0000118; C:histone deacetylase complex; IPI.
GO; GO:0004407; F:histone deacetylase activity; IPI.
GO; GO:0006347; P:chromatin silencing at HML and HMR (sensu S.
GO; GO:0000183; P:chromatin silencing at ribosomal DNA (rDNA);
GO; GO:0006348; P:chromatin silencing at telomere; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a centween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Connor R., Dedman K., Devlin K., Gentles S., Hamlin N Jagels K., Lye G., Moule S., Odell C., Pearson D., Ra Rice P., Skelton J., Walsh S., Whitehead S., Barrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2003 (Rel. 42, Last and Hypothetical 23.0 kDa protein YMR263W OR YM8156.05.
         Spermatophyta; Magn
Asteridae; lamiids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                 Eukaryota;
                                                      LET12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                Homeobox protein
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9169872;
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                                            Lycopersicon
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                             Viridiplantae;
                                                                                                                                                                                                                                                                          201 AA;
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                                                                           (Rel.
(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                      protein
                                            esculentum (Tomato).
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31
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                    Magnoliophyta;
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l. 41, Last e
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          Solanales;
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    Streptophyta; Embryop....
Streptophyta; Embryop....
yta; eudicotyledons; core
yta; eudicotyledons; Solanum
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t annotation of
1 like LET12.
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e EMBL/GenBank/DDBJ databases
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C -> S (II
N -> S (II
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Pred. No.
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les S., Ham
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                                                                            update
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                               Embryophyta; Tracheophyta;
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                     core eudicots
                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                   Length 201;
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RESULT 40
KLP3_SCHPO
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Best Local
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InterPro; IPR005539; ELK.
InterPro; IPR001356; Homeobox.
InterPro; IPR005540; KNOXI.
InterPro; IPR005541; KNOX2.
Pfam; PF03789; ELK; 1.
Pfam; PF03790; KNOX1; 1.
Pfam; PF03791; KNOX2; 1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=cv. VFNT Cherry;
STRAIN=98145476; PubMed=9484482;
MEDLINE=98145476; PubMed=9484482;
Tanssen B.J., Williams A., Chen J.
                                                                                                                                                              SCHPO
                                                                                                                                                                                                                                                                              DOMAIN
DNA BIND
SEQUENCE
                                                                                          KLP3_SCHPO STANDARD; PRT; 5
Q9US60; Q9US61;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Kinesin-like protein 3 (Kinesin-relate
KLP3 OR KRP1 OR SPAC1834.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN THE MATURE
-!- SIMILARITY: BELONGS TO THE TALE/KNOX HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from tomato.";
Plant Mol. Biol. 36:417
-!- FUNCTION: MAY HAVE
          STRAIN=972;
MEDLINE=20109189;
                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                             Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF000142; AAC49918.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of two
                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                 DNA-binding;
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                                                                                                                                                                                                                       742
                                                                                                                                                                                                                                                                                                                                                                               SM00389;
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larity 100.0%;
Conservative
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283
325
349
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15 24
69 76
140 152
283 287
325 348
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Williams H.P.,
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Y HAVE A ROLE TO
          PubMed=10641037;
                                                                                                                                                                                                                                                                                47581 MW;
                            FUNCTION, AND SUBCELLULAR LOCATION

k; NucTear protein.
poly-GLN.
poly-ASN.
poly-ASN.
poly-ASP.
BLK DOWAIN.
HOMEOBOX (TALE-TYPE).

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RX MEDLINE-21848401; PubMed=11859360;
RX MEDLINE-21848401; PubMed=11859360;
RA Sgouros J., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gollins M., Connor T., Lones M., Leather S., Huckle E.J., Hunt S., Jagels K.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Raflor R., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mutler-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Gable C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Berr P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Holaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Holaure V., Mottler S.,
RA Galibert M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Panlsen I., Potashkin J.,
"The genome sequence of Schizosaccharomyces pombe.";
RG C., Langer J., Bearyll B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RG J., Langer J., Sarger M., Sarger J., Sarger J., Sarger J., Sarger J., Sarger J., Sarger J., Sarger
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EMBL; AF25966; AAF22609.1; -.
EMBL; AF247188; AAF81205.1; -.
EMBL; AF247188; CAB75775.1; -.
EMBL; AIL57734; CAB75775.1; -.
PIR; T50118; T50118.
HSSP; P33176; 1BG2.
GeneDB SPOmbe; SPAC1834.07; -.
InterPro; IPR001752; kinesin mot Pfam; P700225; kinesin; 1.
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PROSITE; PS50
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Jeong J.W., Rhee D.K., Cho S.Y., Hae K.L., Kim D.U.,
"Cloning and characterization of the kinesin-related
in Schizosaccharomyces pombe.";
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Yeast 16:149-166(2000).
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n, Krplp,
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SQ SEQUENCE 554 AA, 61918 MW; B4531BD095C49CBD CRC64;

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Marches 13, Conservative 0, Mismarches 0; Indels 0; Gaps 0;

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| 784                  | 772   | 770   | 765   | 751<br>757   | 745   | 743  | 725  | 718   | 713<br>717   | 710  | 678   | 677   | 677   | 673   | 668   | 663  
   | 657  | 652   | 650   | 650  | 634  | 605  | 605   
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   | ABB57783   | AAW18010  | ABP68957  | AAM93793   | ABB71624   | AAB72308   | AAE04789  
  | ABU11606   | ARPR1457   | AAY76811                                     | AAR73935   | AAR11920             | ABP25491   | AAG38679  | ABU02325   
   | AAW69223   | ABB70472            | AAG84948                  | AA014997   | ABBSBSIS   | ABB58106           | ABB70528   | ABJ11360               | ABP73734  
   | ABG91725  | AAG39697   | AAG30660   | ABB70861   | AAB07288                        | ABB61392                        | ABB93400<br>AAM47592   
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| Drosop               | Arabid                                      | dosord  | Drosop  | GGPD.  | Drosop  | Drosop   | Arabid   | Drosop  | Plasmo   | Candid   | D. mel  | Drosop  | Drosop  | Drosop  | Drosop  | Duat-s   
   | Drogop   | Plasmo  | Human   | Human  | Drosop   | Neoxan   | Lycope  
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   | 76   | 766                 | 764                       | 763  | 763  | 760                | 759  | 758                    | 75.5  
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   | 0.6 1182 22  | 0.6 1173 22   | 0.6 1157 22   | 0.6 1152 21  | 0.6 1132 21  | 0.6 1108 22  | 0.6 1058 22   
  | 0.6 1045 21  | 0.6 1037 22  | 0.6 1028 22                                  | 0.6 1015 23  | 0.6 1008 22          | 0.6 998 22   | 0.6 984 20  | .6 984 15  
   | .6 984 13  | 0.6 984 13          | 0.6 976 22                | 0.6 970 23   | 0.6 959 22   | .6 945 23          | .6 944 21  | .6 938 22              | 0.6 916 22  
   | 0.6 900 22  | 0.6 893 22   | 0.6 880 22   | 0.6 865 23   | 0.6 865 23                      | 0.6 854 22                      | 0.6 850 22   
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| .6 1412 22           | .6 1402 23                                  | .6 1398 21  | .6 1316 22  | .6 1278 21<br>6 1311 22  | .6 1247 21  | .6 1242 24<br>.6 1243 16   | .6 1242 24   | .6 1242 24  | .6 1242 24<br>.6 1242 24   | .6 1242 24   | .6 1242 22  | .6 1242 20<br>6 1343 30   | .6 1238 22  | 0.6 1205 23   | 0.6 1205 21   | 0.6 1205 20  
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   | .6 984 13  | 0.6 984 13          | 0.6 976 22                | 0.6 970 23   | 0.6 959 22   | .6 945 23          | .6 944 21  | .6 938 22              | 0.6 916 22  
   | 0.6 900 22  | 0.6 893 22   | 0.6 880 22   | 0.6 865 23 ABP356  | 0.6 865 23 ABP356               | 0.6 854 22 AAG673               | 0.6 850 22 ABB657  
   | 0.6 814 22 ABB65  | 0.6 812 21 AAY95   | .6 811 22 ABG231   | .6 798 22 ABB623   | .6 787 23 ABB082<br>.6 797 20 AAY058   
   |
| .6 1412 22           | .6 1402 23                                  | .6 1398 21  | .6 1316 22  | .6 1278 21<br>6 1311 22  | .6 1247   | .6 1242 24<br>.6 1243 16   | .6 1242 24   | .6 1242 24  | .6 1242 24<br>.6 1242 24   | .6 1242 24   | .6 1242 22  | .6 1242 20<br>6 1343 30   | .6 1238 22  | 0.6 1205 23   | 0.6 1205 21   | 0.6 1205 20  
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  | 0.6 1045 21  | 0.6 1037 22  | 0.6 1028                                     | 0.6 1015 23  | 0.6 1008 22          | 0.6 998 22   | 0.6 984 20  | .6 984 15  
   | .6 984 13  | 0.6 984 13          | 0.6 976 22                | 0.6 970 23   | 0.6 959 22   | .6 945 23          | .6 944 21  | .6 938 22              | 0.6 916   
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| .6 1412 22 ABB60943  | .6 1402 23 ABP66040                         | .6 1398 21 AAB18292   | .6 1316 22 ABB69263   | .6 1278 21 AAB18277<br>6 1311 22 ABB61234  | .6 1247 21 AAB18215   | .6 1242 24 ABG/23/2<br>.6 1243 16 AAR67708   | .6 1242 24 ABG72371  | .6 1242 24 ABG72370   | .6 1242 24 ABG72368<br>.6 1242 24 ABG72369   | .6 1242 24 ABB99797  | .6 1242 20 AAB83921   | .6 1242 20 AAY13461<br>6 1242 20 AAY13472   | .6 1238 22 ABB61259   | 0.6 1205 23 AAO21863  | 0.6 1205 21 AAW90882  | 0.6 1200 22 ADB03333   
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  | 0.6 1045 21 AAG45672   | 0.6 1037 22 ABB70288   | 0.6 1028 22 ABB62708<br>0.6 1032 21 AAG45673 | 0.6 1015 23 ABP73325   | 0.6 1008 22 ABB59260 | 0.6 998 22 ABB60423  | 0.6 984 20 AAY29589   | .6 984 15 AAR60164   
   | .6 984 13 AAR27529   | 0.6 984 13 AAR22247 | 0.6 976 22 ABB65498       | 0.6 970 23 ABP35631  | 0.6 959 22 AAG64950  | .6 945 23 ABP73277 | .6 944 21 AAB43351   | .6 938 22 ABB60562     | 0.6 916 22 ABB63615 L   
   | 0.6 900 22 ABB60688   | 0.6 893 22 ABB64865  | 0.6 880 22 AAR70938  | 0.6 865 23 ABP35642  | 0.6 865 23 ABP35641             | 0.6 854 22 AAG67391             | 0.6 850 22 ABB65764  
   | 0.6 814 22 ABB65317   | 0.6 812 21 AAY95985  | .6 811 22 ABG23352   | .6 798 22 ABB62356   | .6 787 23 ABBO8247 . H<br>.6 797 20 AAY05850 B   
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| .6 1412 22 ABB60943  | .6 1402 23 ABP66040 Bif                     | .6 1398 21 AAB18292   | .6 1316 22 ABB69263   | .6 1278 21 AAB18277<br>6 1311 22 ABB61234  | .6 1247 21 AAB18215 Plasmod   | .6 1243 16 AAR67708 Insulin  | .6 1242 24 ABG72371 Human  | .6 1242 24 ABG72370 Human   | .6 1242 24 ABG72368 Human<br>.6 1242 24 ABG72369 Human   | .6 1242 24 ABB99797 Amino  | .6 1242 22 AAB83921 Amino   | .6 1242 20 AAY13461 Amino   | .6 1238 22 ABB61259   | 0.6 1205 23 AAO21863  | 0.6 1205 21 AAW90882  | 0.6 1200 22 ADB03333   
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  | 0.6 1045 21 AAG45672   | 0.6 1037 22 ABB70288   | 0.6 1028 22 ABB62708<br>0.6 1032 21 AAG45673 | 0.6 1015 23 ABP73325   | 0.6 1008 22 ABB59260 | 0.6 998 22 ABB60423  | 0.6 984 20 AAY29589   | .6 984 15 AAR60164   
   | .6 984 13 AAR27529   | 0.6 984 13 AAR22247 | 0.6 976 22 ABB65498       | 0.6 970 23 ABP35631  | 0.6 959 22 AAG64950  | .6 945 23 ABP73277 | .6 944 21 AAB43351   | .6 938 22 ABB60562     | 0.6 916 22 ABB63615 L   
   | 0.6 900 22 ABB60688   | 0.6 893 22 ABB64865  | 0.6 880 22 AAR70938  | 0.6 865 23 ABP35642 Fungai   | 0.6 865 23 ABP35641 Fungal      | 0.6 854 22 AAG67391             | 0.6 850 22 ABB65764  
   | 0.6 814 22 ABB65317   | 0.6 812 21 AAY95985  | .6 811 22 ABG23352   | .6 798 22 ABB62356   | .6 787 23 ABBO8247 . H<br>.6 797 20 AAY05850 B   
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| .6 1412 22           | .6 1402 23 ABP66040 Bif                     | .6 1398 21 AAB18292   | .6 1316 22  | .6 1278 21 AAB18277<br>6 1311 22 ABB61234  | .6 1247 21 AAB18215 Plasmodium  | .6 1243 16 AAR67708 Insulin  | .6 1242 24 ABG72371 Human  | .6 1242 24 ABG72370 Human   | .6 1242 24 ABG72368<br>.6 1242 24 ABG72369   | .6 1242 24 ABB99797 Amino  | .6 1242 22 AAB83921 Amino acid  | .6 1242 20 AAY13461 Amino acid  | .6 1238 22 ABB61259   | 0.6 1205 23 AAO21863  | 0.6 1205 21 AAW90882  | 0.6 1200 22 ADB03333   
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AAM62493
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AAM60044
AAM72647
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ABG42471
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AAO04685
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Arabidopsis thalia
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Arabidopsis thalia
Human liver peptid
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Peptide #2953 enco
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Peptide #2893 enco
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Peptide #9452 enc
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Peptide #9128 enco
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                    Kappler JW,
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  The sequences given in AAR41990-2013 are mutant versions Staphylococcus enterotoxin B (SEB) super antigen (SAg).
                                                                                                Preventing or treating toxic effects of super antigens - by admin. of new modified or mutated super antigen which induces antibodies but not T-cell activation
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                                            The sequences given in AAR41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
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; PCR; modify; T-cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxic effects of super antigens - by admin. d super antigen which induces antibodies but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Region undisclosed in
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                 Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAR41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR41997;
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                                               WO9314634-A1
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                                                             or treating
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                                                                                                       Marrack
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(first entry)
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                                                                                                                                                                                                                                                                                                aureus.
                                                                                                                                                                                                                                                                                                                                                              enterotoxin
                                                                                                                                                 92US-0827540.
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                                                                                                                                                                                                                                                                 Location/Qualifiers 97..157
                                                                                                                                                                                                                                             162..186
                                                                                                                                                                                                                                   note=
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                                                    toxic effects of super antigens -
d super antigen which induces antil
                                                                                                                                                                                                                                   "Region undisclosed in the
                                                                                                                                                                                                                                                      "Region undisclosed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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                                                                                                                                                                                                                                                                                                                                                             B mutant
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Pred. No.
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1.2e-07;
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T-cell
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Disclosure;

Fig 3; 54pp;

English

sequences given in

AAR41990-2013

are mutant versions

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the

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RESULT 12
AAR42000
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Best Local S
Matches 17
                                           Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutary generated by random mutation by PCR, may be used to modify the T-cer response ellcited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-
                                                                             Disclosure; Fig 3; JPF, L...

The sequences given in AAR41990-2013 are mutant versions of the mutants of the sequences given in AAR41990 super antigen (SAg). These mutants are modify the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutar generated by random mutation by PCR, may be used to modify the T-cel response elicited by an antigen. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
                                                                                                                                                        Preventing or treating toxic effects of super antigens - by admew modified or mutated super antigen which induces antibodies not T-cell activation
                                                                                                                                                                                                                                                                                                                                                            WO9314634-A1
                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus enterotoxin B mutant BA-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
21-APR-1994
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                   Vbeta types.
                                reactive T-cells may be
                                                                                                                                                                                                          WPI; 1993-320314/40
                                                                                                                                                                                                                                   Kappler
                                                                                                                                                                                                                                                           (NAJE-)
                                                                                                                                                                                                                                                                                    28-JAN-1992;
                                                                                                                                                                                                                                                                                                           28-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation;
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                                                                                                                                                                                                                                   JW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease.
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          25-MAR-2003
                                                                                                                                                                                                                                                           JEWISH CENT
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97..157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; modify;
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                                 activated by
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          correct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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          PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             super antigen; SAg; receptor;
l; response; antigen; Vbeta el
                                SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; I
1.2e-07;
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y the T-cell
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AAR42001
ID AAR42
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Best Local S
Matches 17
                                  Query Match
Best Local Similarity
Matches 17; Conserv
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21-APR-1994
                                                                                                                  The sequences given in AAR41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
                                                                              Sequence
                                                                                                                                                                                                                        Preventing or treating toxic effects of super antigens - new modified or mutated super antigen which induces antik not T-cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                    Disclosure; Fig 3; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus enterotoxin B mutant
                                                                                                                                                                                                                                                                                                                               28-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                   28-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                           (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                         WO9314634-A1
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                                                                                                  (Updated
 171
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           g
 INNNNNNNNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNNNNNNNNNNNN 187
                                                                              190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease.
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                                     1.3%;
ilarity 100.0%;
Conservative (
                                                                                                   25-MAR-2003
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(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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                                                                                                                                                                                                                                                                                       70
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 187
                                                                                                   correct PN field.)
                                      0;
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                                                 Score 17;
Pred. No.
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Pred. No.
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                                        Mismatches
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                                               DB 14; 1
1.2e-07;
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1.2e-07;
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                                                         Length 190;
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RESULT 14
AAR42002
RESULT 15
AAR42003
ID AAR42
XX
AC AAR42
XX
DT 25-MA
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                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
21-APR-1994
                                                                                                                                                                                                                                    The sequences given in AAR41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
                                                                                                                                                                                                                                                                                                                                                   Preventing or treating toxic effects of super antigens - by adn new modified or mutated super antigen which induces antibodies not T-cell activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                random mutation; PC autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR42002;
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                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                    Kappler JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
  25-MAR-2003
                                             AAR42003 standard;
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-320314/40
                                                                                                                                                                                                                                                                                                                                                                                                                                            (NAJE-) NAT
                        AAR42003;
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                                                                                                                         742
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                                                                                                                        NNNNNNNNNNNNN 758
                                                                                                    NNNNNNNNNNNNN 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                            JEWISH CENT IMMUNOLOGY & RESPIRATORY
                                                                                                                                                                                                                                                                                                                             Fig 3; 54pp; English.
                                                                                                                                               Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Region undisclosed 162..186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                             protein; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          otoxin B; SEB; super antigen; SAg; receptor;
modify; T-cell; response; antigen; Vbeta element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Region undisclosed in
                                                                                                                                                                                                                to correct PN field.)
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                                                                                                                                                          Score 17; DB 14;
; Pred. No. 1.2e-07;
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                                                                                                                                                 Mismatches
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망 á

Staphylococcus aureus

autoimmune

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RESULT 16
AAAR42004
ID AAR42
XX AAR42
AC AAR42
AC AAR42
XX 25-MB
DT 25-MB
DT 21-AB
XX Staph
XX Staph
KW randd
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preventing or treating toxic effects of super antigens - by adr
new modified or mutated super antigen which induces antibodies
not T-cell activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease.
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                                                    Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor; random mutation; PCR; modify; T-cell; response; antigen; Vbeta el
                                                                                                           Staphylococcus enterotoxin B mutant BA-53.
                                                                                                                                                  25-MAR-2003
21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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21-APR-1994
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Kappler JW,
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162..1
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d super antigen which induces antibodies
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                      The sequences given in AAR41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
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J. 1.2e-07;
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                                                                                                    The sequences given in AAR41990-2013 are mutant versions of the Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants generated by random mutation by PCR, may be used to modify the T-cell response elicited by an antigen, by interacting with specific Vbeta elements of the T-cell receptors. This T-cell response modulation may be useful in a wide variety of autoimmune diseases, where self-reactive T-cells may be activated by SAg that bind to particular
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Pred. No.
                                      Score 17; DB 14;
Pred. No. 1.2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEB; super antigen; SAg; receptor; T-cell; response; antigen; Vbeta element;
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                             Mismatches
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. 1.2e-07;
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RESULT 23
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RESULT 22
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21-APR-1994
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1.2e-07;
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21-APR-1994
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                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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RESULT 27
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22-OCT-1999;
22-OCT-1999;
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20-FEB-2001;
22-AUG-2001;
The invention relates to constructing (MI) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifyione allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (MI) is useful for constructing a strain of diploid fungal
                                                                                                                                                                                                                                                                                                                                                 Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal.
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26-OCT-1999;
                                                                                                     expression
                                                                                                              of a gene and
                                                                                                               Constructing strains for identifying gene products as for therapeutic intervention, by inactivating in the sof a gene and placing other allele of the gene under of
                                                                                                                                                        N-PSDB;
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2001US-0792024.
2001US-314050P.
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99US-0160814.
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03-JUL-1991;
27-NOV-1991;
                                                                                                                                                       New polypeptide(s) derived from human fibronectin - promote attachment to substrates, inhibit platelet aggregation and thrombus formation and modulate coagulation and inflammatory
                                                                                                                                                                                                                                                                                     WPI;
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AAQ25592 comprises bps 901-1506 of a

human fibronectin

(Fn) encoding

DNA

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RESULT 30
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AC AAY72
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                                                                                                                                                                                                                                                                                                                                           EP1078985-A2
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                                 Claim 11;
                                                                           Novel nucleic acids encoding plant-mitogen activated kinase kinase derivative which has negative charge at core phosphorylation site, useful for enhancing stress tolerance or increasing disease resists
                                                                                                                                                                                                                                           27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation_site
                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tolerance; signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PN field.)
                                                                                                                                                                             Miki BL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VII and VIII"
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                                                                               resistance
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The present invention relates to a derivative of plant mitogen-activated

Proteins AAW02657-W02720 represent a range of G-protein coupled receptor (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endochelin, bombesin, endocrine, rhodopsin, opsin, odorant, cytomegaloviral and other GPR proteins. The peptides AAW03578-W03651 represent the N-terminal fragments of the above proteins. The receptor proteins were used to design polypoptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor

coupled receptor

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RESULT 31
AAW03625
ID AAW03
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Best Local
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                                                                                                                                                                                                   Murphy RB,
                                                                                                                                                                                                                                                                                                                                                                                                                    muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein coupled receptor; ligand binding assay; transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
17-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase kinase (MAPKK or MEK) which contains a negative charge the core phosphorylation site of MAPKK. MAPKK activates MAPK signalling cascades which are ubiquitous among eukaryotes from yeast to human and mediate a large array of signal transduction pathways in plants.
                                                                                                      Disclosure; Fig 8B(2); 184pp; English.
                                                                                                                                                                       WPI; 1996-208785/21.
                                                                                                                                                                                                                                                      09-SEP-1993;
10-SEP-1992;
                                                                                                                                                                                                                                                                                               09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                    US5508384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lutropin-choriogonadotropin GPR N-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW03625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW03625 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: This sequence designated as SEQ ID NO: 6 is stated same as that shown in sequence listing (AAY72779) of the However, the sequences differ at several positions.
                                                                                                                                                                                                                                                                                                                          16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   schizophrenia;
                                                                                                                                                                                                                             (UYNY ) UNIV NEW YORK STATE
                                                                                                                                 or treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAPKK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  742 NUNNNNNNNNNNNN 757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     acetylcholine;
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                                                                                                                                                                                                   Schuster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (updated)
(first en
                                                                                                                                            receptor peptide - useful as antipsychotic agent,
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92US-0943236.
                                                                                                                                                                                                                                                                                               93US-0118270
                                                                                                                                                                                                                                                                                                                                                                                                                                   dopamine; cAMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide; 342
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tive 0;
                                                                                                                                                                                                   PI,
                                                                                                                                                                                                                                                                                                                                                                                                       cAMP; adenosine; thrombin; adrenergic; opsin
endothelin; bombesin; endocrine; rhodopsin;
serotonergic.
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hes 0;
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RESULT 32
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Matches 16
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19-MAR 1999

23-MAR 1999

25-MAR 1999

26-APR 1999

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(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000;
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cal Similarity 100.0%;
16; Conservative
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Pred. No.
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AAO19019 standard; Protein; 357
                                                                                                                                                                                                                                                                                                       The present invention describes fusion proteins (I) comprising at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis, at least one hydrophilic polypeptide having no immunoreactivity to human serum and their connected part. AAA08120 to AAA08125 encode specifically claimed examples of the fusion proteins given in AAY82388 to AAX82393. Also described is a method (A) for the detection of Chlamydia trachomatis antibody using (I) as the antigen. (I) is used for the diagnosis of Chlamydia trachomatis infectious diseases. The method can diagnose Chlamydia trachomatis infectious diseases specifically in a can diagnose Chlamydia trachomatis infectious diseases
                                                                                                                                                                                                                                                     Sequence
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N-PSDB; AAA08124.
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                                                                                                 168
                                                                                                                                                                                                                                                                                         sensitivity.
                                                                                                                                     742 NNNNNNNNNNNNNN 757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 24-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e fused protein us at least part of a trachomatis -
                                                                                                 NNNNNNNNNNNNN
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     WPI; 2002-664560/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan; kinesin motor protein; HsKifl6a; motor domain; microtubule-stimulated ATPase activity; adenosine triv
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neurological disorder; vesicular transport disorder; autoimmune dis
arthritis; graft rejection; proliferation; cytostatic; neurotropic;
immunosuppressive; antiarthritic; antiinflammatory.
                                                               New human kinesin motor protein, HsKif16a, having microtubule-stimulated ATPase activity, useful for identifying specific
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                                                                                                                                           N-PSDB;
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larity 100.0%;
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Claim 3; Fig 4; 27pp; English

modulators for

e.g. treating cancer

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RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a human kinesin motor protein, HsKif16a, comprising a motor domain and having microtubule-stimulated APPase (adenosine triphosphatase) activity. The protein of the invention and its associated nucleic acid are useful in diagnosis, treatment and prevention of cancer, neurological disorders, disorders of vesicular transport, autoimmune diseases, arthritis, graft rejection, inflammation and proliferation induced after medical procedures. The protein is also used to identify its specific modulators, potentially useful as therapeutic agents. This sequence represents the motor domain of the HsKifl6a polypeptide of the invention.
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99US-0160.98.
99US-01610.98.
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                                                                  producing chemicals
                                                                          other host cells. The cellulase protein is useful for degrading cellulosic material in textile and paper industries, and also for producing ethanol. Cellulase is also useful for producing fuels an
                                                                                                       The present sequence represents a CelF protein of Orpinomyces sp. PC-2. CelF is a cellulase, which has endoglucanase activity and produces cellobiose from cellotetroase or cellopentoase, and glucose and cellobiose from cellotriose. The CelF polynucleotide is useful for recombinantly expressing CelF mature protein in Escherichia coli or they have tellotriose.
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                                            Sequence
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textile and paper industries, and
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                                                                                                                                                                                                                                         AAB30803-17 represent prion-like amyloidogenic proteins which have been identified from a yeast protein database. The specification describes chimeric polypeptides, which comprise at least one SCHAG (self-coalesces into higher-order aggregates) amino acid sequence in frame with a polypeptide of interest (which is other than a mari protein, a glutathione-S-transferase or a staphylococcal nuclear
                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding chimeric proteins with sel
properties, useful e.g. for diagnosis and treatment
also related aggregates, fibrils and polymers -
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                                                                                     Sequence
                                                                                                              in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases.
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                                                                  Sequence
                                                                                          prevent cancer, immune disorders, inflammation, neurological disorders and disorders of vesicular transport. The present sequence is the protein
                                                                                                  The present invention provides the protein and coding sequences of a human motor protein which has microtubule stimulated ATPase activity are is designated HSKIFIGA. The nucleic acid is used to diagnose, treat and prevent cancer, immune disorders, inflammation, neurological disorders
                                                                                                                                                            New nucleic acid encoding a motor protein which has microtubule stimulated ATPase activity, designated HSKIF16A, for preventing attreating cancer, and neurological and vesicle transport disorders
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Sequence 6, Application US/09384162

Patent No. 6376747

GENERAL INFORMATION:
APPLICANT: Xing, Ti
APPLICANT: Malik, Kamal
APPLICANT: Malik, Kamal
APPLICANT: Makik, Kamal
APPLICANT: Miki L., Brian
APPLICANT: Miki L., Brian
CURRENT FILLERSTION: No. 6376747el Plant-Derived Map Kinase Kinase
FILE REFERENCE: O8-884280US
CURRENT APPLICATION NUMBER: US/09/384,162

CURRENT FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 286
TYPE: PRT
ORGANISM: Dictyostelium discoideum
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6333184el motor
TITLE OF INVENTION: their use
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RESULT 4
US-09-118-319-5
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; NAME/KEY: VARIANT
; LOCATION: (16)...(37)
; OTHER INFORMATION: Xaa = any amino acid
US-09-718-810-4
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US-09-718-810-4
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                            US-09-118-319-5
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                                                                                                          Sequence 5, Application US/09118319

Patent No. 614158

GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Orpinomyces Cellulase CelF Protein and Coding:
FILE REFERENCE: 33-98sequence listing
CURRENT APPLICATION UNMERS: US/09/118,319

CURRENT FILING DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/718,810
CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 16
                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09718810 Patent No. 6420162
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Best Local
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 357
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
FEATURE:
NAME/KEY: VARIANT
LOCATION: (16)...(37)
OTHER INFORMATION: Xaa = any amino acid
                                         LENGTH: 428
TYPE: PRT
ORGANISM: Neocallimastix patriciarum
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16; Conservative (
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100.0%; Pr
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Pred. No.
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Pred. No.
 Score 16;
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Length 428;
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US-09-118-319-2
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US-09-118-319-2
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; SEQ ID NO 2
; LENGTH: 563
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APPLICANT: Li, Xin-Liang
APPLICANT: Chen, Huizhong
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Orpinomyces Cellulase Celf Protein and Coding Sequences
FILE REFERENCE: 33-98sequence listing
CURRENT APPLICATION NUMBER: US/09/118,319
CURRENT APPLICATION NUMBER: US/09/118,319
CURRENT FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
I ENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: Christophe APPLICANT: Beraud, Christophe APPLICANT: Freedman, Richard APPLICANT: No. 62271
                                                                  Matches
                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09718841 Patent No. 6333184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Patent No. 6114158
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                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 1051
CURRENT APPLICATION NUMBER: US/09/718,841
CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6333184el motor proteins
TITLE OF INVENTION: their use
                                                                                                                                         NAME/KEY: VARIANT
LOCATION: (16)...(37)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
LOCATION: (391)...(412)
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 432
TYPE: PRT
ORGANISM: Orpinomyces sp. PC-2
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                 92 FAYGQTGSGKTYTMLG 107
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16; Conserv
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FAYGQTGSGKTYTMLG 113
                                                             1.2%; Sc
llarity 100.0%; P
Conservative 0;
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Pred. No. 3.8e-07;
                                                                              Score 16;
Pred. No.
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                                                                Mismatches
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US-09-718-810-2
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CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.1
SEQ ID NO 2
LENGTH: 563
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Beraud, Ch
APPLICANT: Freedman,
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Patent No. 6346406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09718810 Patent No. 6420162
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEY: VARIANT
LOCATION: (16)...(37)
OTHER INFORMATION: Xaa = a
NAME/KEY: VARIANT
LOCATION: (391)...(412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 642010
                                                                                                                                                                                                                                                                                          STREET: **-
STREET: Floor
STREET: Floor
CITY: Hackensack
~~~TE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                  APPLICATION NUMBER: US/08/914,999
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ryazanov, Alexey G. APPLICANT: Hait, William N. APPLICANT: Pavur, Karen S.
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                 REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 07601
TELEPHONE:
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Freedman, Richard
VENTION: No. 6420162el motor proteins
                                                                                                                                                                                                                                                                                                                                                                          411 Hackensack Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                            David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELONGATION FACTOR-2 KINASE (EF-2 KINASE) AND METHODS OF USE THEREFOR
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Continental Plaza, 4th
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                                                                                                      US-08-340-011-5
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Sequence 5, App...
Sequence 5, App...
                                                                 Query Match
Best Local
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                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9
FILING DATE: 09-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                     MOLECULE TYPE:
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                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                             NAME: Meyers, Thomas REGISTRATION NUMBER:
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                                                 1.2%; Score 16; llarity 100.0%; Pred. No. Conservative 0; Mismatch
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100.0%; Pr
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FIT4, A NOVEL RECEPTOR TYROSIN KINASE
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628
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Pred. No.
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6.1e-07;
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RESULT 10
US-08-901-710-5
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US-09-457-040B-27
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Sequence 27, Application US/09457040B Patent No. 6387641
GENERAL INFORMATION:
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Patent No. 610704
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
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PRIOR APPLICATION UMBER: 08/340,011
FILLING DATE: 14-NOV-1994
PRIOR APPLICATION NUMBER: 08/257,754
APPLICATION NUMBER: 08/257,754
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 312/474-6300
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TOPOLOGY: 1i
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TVDE; amino acid
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6300 Sears Tower, 233
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Korhonen, Jaana
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Aprelikova, Olga
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09-0CT-1992
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100.0%; Pr
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0; Mismatches
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South Wacker Drive
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APPLICANT: Vertex Pharmaceuticals Incorporated

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APPLICANT: Bellon, Steve
TITLE OF INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VPI/98-14
CURRENT APPLICATION UMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 1584
TYPE: PRT
ORGANISM: DICDI - Dictyostelium Discoideum
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SOFTWARE: Fa
SEQ ID NO 4
LENGTH: 303
                                                                                                          GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6582958el motor proteins and methods for
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
FILE REFERENCE: 47714-5009-US
CURRENT APPLICATION NUMBER: US/09/417,485D
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 2184
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Best Local
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APPLICANT: Long, David M.
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                                                  FILE REFERENCE: 1054
CURRENT APPLICATION NUMBER: US/09/722,129
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 4
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16; Conserv
                                 FastSEQ for Windows Version 4.0
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100.0%; Pred. No.
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US-09-417-485D-8
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US-09-722-129-2
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LENGTH: 492
TYPE: PRT
ORGANISM: Human
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APPLICANT: Long, David M.
APPLICANT: Long, David M.
APPLICANT: Metz, Anneke M.
APPLICANT: Love, Ruschelle A.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
FILE REFERENCE: 47714-5009-US
CURRENT APPLICATION UNMEER: US/09/417,485D
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 794
TYPE: PRT
ORGANISM: Plasmodium falciparum
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
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                                                       Local Similarity
nes 15; Conserv
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NNNNNNNNNNNN 144
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                                                         conservative 0;
                                                                       1.2%; Score 15;
100.0%; Pred. No.
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                                                                       DB 4; Le
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RESULT 16 US-08-861-464-6

; Sequence 6, Application US/08861464

Patent No.

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RESULT 17
US-08-396-001-6
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Best Local (
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                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Guaren
APPLICANT: Austri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 781-861-9540 INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,464
FILING DATE: 22-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US94/09351
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 04
FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kennedy, TITLE OF INVENTION: TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                  APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining
TITLE OF INVENTION: Yeast
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/107,408 FILING DATE: 16-AUG-1993
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Austriaco Jr., Nicanor
                                                                                                                  Claus, James
Cole, Francesca
                                                                                                                                                 Guarente, Leonard P.
Austriaco Jr., Nicanor
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100.0%; Pred. No.
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                 Smith & Reynolds, P.C
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lo. 6.9e-06;
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; MOLECULE TYPE:
US-08-396-001-6
                                                                                                                        ; LENGTH: 888
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-323-433A-6
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                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 6
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                                                               Matches
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                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                          FITEE OF INVENEZACION OSS. 1491-003
FILE REFERENCE: 0050.1491-003
CURRENT APPLICATION NUMBER: US/09/323,433A
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: US 08/396,001
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/
PRIOR TILING DATE: 1994-08-18
PRIOR APPLICATION NUMBER: US 0
PRIOR FILING DATE: 1993-08-16
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1995-0
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kennedy, Brian
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: YEAST
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                   742 NNNNNNNNNNNNNN 756
521 NNNNNNNNNNNNN 535
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Cole, Francesca
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UMBER: US 08/107,408
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                                                                            Score 15;
Pred. No.
                                                               Mismatches
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                                                                 Indels
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US-09-098-901-11

Application US/09098901B

Sequence 11, Applica Patent No. 6218144 GENERAL INFORMATION:

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RESULT 21
US-09-723-129-4
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; LOCATION: (1)...(23)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-098-901-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-641-806-4
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                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6395527el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 23
                                                                         Sequence 4, Application US/09723129
Patent No. 6551787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 4, Application US/09641806
Patent No. 6395527
                                                             GENERAL INFORMATION:
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Best Local (
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Best Local Similarity
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6551787el motor proteins and methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/098,901B
CURRENT FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: 60/051,347
EARLIER FILING DATE: 1997-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/641,806
CURRENT FILING DATE: 2000-08-17
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APPLICANT: Sisson, John C.
TITLE OF INVENTION: Costal2 Genes and their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: SUN-65P
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ORGANISM: CONSENSUS
FEATURE:
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 337
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100.0%; Pred. No.
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Pred. No.
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; ORGANISM: Human
US-09-641-806-2
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US-09-722-862-4
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                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
                                                                                                            APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6395527el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1034
CURRENT APPLICATION NUMBER: US/09/641,806
CURRENT FILING DATE: 2000-08-17
NUMBER OF SEC 15 1000-08-17
                                                                                                                                                                                                                                                                      Sequence 2, Application US/09641806 Patent No. 6395527
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Patent No. 6562610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/722,862
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/641,806
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6562610el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1034
                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/641,806
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
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CURRENT FILING DATE: 2000-11-27
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                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 337
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
                                                  LENGTH: 342
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tive 0;
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100.0%; Pred. No. 2.8e-05;
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; LENGTH: 342
; TYPE: PRT
; ORGANISM: Human
US-09-723-129-2
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US-09-723-129-2
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US-09-722-862-2
                                                                                                                            US-09-722-862-2
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CURRENT APPLICATION NUMBER: US/09/723,129
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/641,806
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/722,862
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/641,806
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
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Best Local Similarity
                                                               Matches
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                                                                               Query Match
Best Local
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TITLE OF INVENTION: No. 6562610el motor proteins and methods for
TITLE OF INVENTION: their use
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APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6551787el motor proteins and methods for
TITLE OF INVENTION: their use
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                                                                                                                                          TYPE: PRT
ORGANISM: Human
                                                                                                                                                                           LENGTH: 342
                                                                              Local
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Local Similarity 100.0%; Pred. No. 2.8e-05;
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                             92 FAYGOTGSGKTYTM 105
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FAYGOTGSGKTYTM 94
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100.0%; Pred. No. 2.8e-05;
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                                                                            Score 14; Pred. No.
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RESULT 26

RESULT 28 US-08-006-676B-1

Sequence 1, Application US/08006676B Patent No. 5411865
GENERAL INFORMATION:
APPLICANT: Reed, Steven

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APPLICANT: Vale, Ronald D.

APPLICANT: Hartman, James J.

APPLICANT: Hartman, James J.

APPLICANT: The Regents of the University of California
ITITE OF INVENTION: Assays for the Detection of Microtubule
ITITE OF INVENTION: Depolymerization Inhibitors

FILE REFERENCE: 185578-000510US

CURRENT APPLICATION NUMBER: US/09/724,884

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/291,170

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
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APPLICANT: Hartman, James J.

APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for the Detection of Microtubule
TITLE OF INVENTION: Depolymerization Inhibitors
FILE REFERENCE: 185578-0005510US
CURRENT APPLICATION NUMBER: US/09/291,170A
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 60/081,734
PRIOR APPLICATION NUMBER: US 60/081,734
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Xenopus laevis
; FEATURE:
; OTHER INFORMATION: Xenopus kinesin central motor 1 (XKCM1)
US-09-724-884-3
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LENGTH: 730
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                                                                                                     Query Match
Best Local
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Local Similarity 100.0%; P
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520 INRSLLALKECIRA 533
                            263 INRSLLALKECIRA 276
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                                                                                                     Similarity
                                                                           1.1%; Score 14; DB 4; Lilarity 100.0%; Pred. No. 5.6e-05; Conservative 0; Mismatches 0;
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Pred. No.
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5.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08282845
Patent No. 5719263
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh Operating System
SOFTWARE: Microsoft Word for Macintosh 5.1a
CURRENT APPLICATION DATA:
                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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NAME: OSTET, Jeffrey B.
REGISTRATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: REED-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD for Windows
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acid
             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                              FILING DATE: JANUARY 15, 1993
                                                                                                                 FILING DATE:
                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                   COUNTRY: UZIP: 98101
                                                                                                                                                                                                                                                                                                  CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1: CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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Perkins, Patricia Anne
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15-JAN-1993
ON: 435
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                                                                08/006,676
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; Pred. No. 7.1e-05;
recomptedes 0;
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                                                                                                                      US-08-428-414A-3
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GENERAL INFORMATION:
                                                            Matches
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Best Local S
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Best Local Similarity 100.0%;
                                                                                                                                                                                                               TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Statistic OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                        NAME: Kadlecek, Ann T.
REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       NAME:
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-APR-1995
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/428,414A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
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                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                 ENGTH:
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119 FAYGQTGSGKTYTM 132
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                            92 FAYGOTGSGKTYTM 105
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                                                                         Similarity
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                                                                                                                                    Linear
                                                                                                                                                                                  amino acids
                                                                                                                                                                                                                                                            (206) 622-4900
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                                                         Score 14; DB; Pred. No. 7.1: 0; Mismatches
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Pred. No.
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                                                                                      Length 955,
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PCT-US94-00324-1

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US-09-724-517-4
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                Query Match
 Best Local Similarity
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APPLICATION NUMBER: US/08/006,676
APPLICATION NUMBER: US/08/006,676
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-WO
                                                                                                                                                                                                                                                                 APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6379941el motor proteins and methods for
TITLE OF INVENTION: their use
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/724,517
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US/09/641,807
PRIOR FILING DATE: 2000-08-17
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  FILE REFERENCE: 1031
                                                                    LENGTH: 341
TYPE: PRT
ORGANISM: Human
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word, version:
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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Local Similarity 100.0%; I
nes 14; Conservative 0;
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CITY: Seattle
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1.0%;
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Score 13;
Pred. No.
DB 4; L
                  Length 341;
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RESULT 35
US-09-177-165A-31
; Sequence 31, Application US/09177165A
; Patent No. 6426205
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APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6448026el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1031
CURRENT APPLICATION NUMBER: US/09/723,096
CURRENT APPLICATION NUMBER: US/09/641,807
PRIOR APPLICATION NUMBER: US/09/641,807
PRIOR FILING DATE: 2000-08-17
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Best Local Similarity 100.0%;
Conservative (
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Best Local 9
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/641,807A
CURRENT FILING DATE: 2000-08-17
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APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6440731el motor proteins and methods for
TITLE OF INVENTION: their use
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ORGANISM: Human
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TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                     Match 1.0%; Sc
Local Similarity 100.0%; F
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GENERAL INFORMATION:

APPLICANT: Tyers, Mike

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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (409)...(436)
; OTHER INFORMATION: Xaa = any amino acid
US-09-724-517-2
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US-09-641-807A-2
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PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1279
                                   GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6440731el motor proteins and methods for
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 1151
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.10USU1
CURRENT APPLICATION NUMBER: US/09/177,165A
CURRENT FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR APPLICATION NUMBER: 60/063,254
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
                                                                                                                                              Sequence 2, Application US/09641807A Patent No. 6440731
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TITLE OF INVENTION: No. 6379941el motor proteins and methods for
TITLE OF INVENTION: their use
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CURRENT FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beraud, Christophe APPLICANT: Freedman, Richard
CURRENT APPLICATION NUMBER: US/09/641,807A
                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
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100.0%; Pred. No. 0.00088;
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; FEATURE:
, NAME/KEY: VARIANT
; LOCATION: (409)...(436)
; OTHER INFORMATION: Xaa = any amino acid
US-09-723-096-2
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for W
SEQ ID NO 2
LENGTH: 1279
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                                                                                                                                                                                                                                                    US-09-451-117-2
                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jenkins, Mark C.
APPLICANT: Fayer, Ronald
APPLICANT: Trout, James
                                                                 TITLE OF INVENTION: Cloning and Expression of a DNA Sequence Encoding A 41 Patent No. 6277973
TITLE OF INVENTION: kDa Cryptosporidium parvum Oocyst Wall Protein FILE REFERENCE: 0046.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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Patent No. 6277973
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Patent No. 6448026
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/723,096
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US/09/641,807
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
                CURRENT APPLICATION NUMBER: US/09/451,117
CURRENT FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Freedman, Richard TITLE OF INVENTION: No. 6448026el motor proteins and methods for TITLE OF INVENTION: their use
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SOFTWARE: PatentIn Ver. 2.1
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NAME/KEY: VARIANT
LOCATION: (409)...(446)
OTHER INFORMATION: Xaa = any amino acid
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ORGANISM: Humain
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100.0%; Pred. No.
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Pred. No. 0.00088
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Sequence 2. Application US/09888655

Patent No. 6521229

GENERAL INFORMATION:
APPLICANT: Jenkins, Mark C.
APPLICANT: Fayer, Ronald
APPLICANT: Trout, James
TITLE OF INVENTION: Cloning and Expression of a DNA Sequence Encoding A 41
Patent No. 6521229
TITLE OF INVENTION: MDA Cryptosporidium parvum Oocyst Wall Protein
FILE REFERENCE: 0046.99
CURRENT APPLICATION NUMBER: US/09/888,655
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Cryptosporidium parvum
US-09-888-655-2
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LENCTH: 246
TYPE: PRT
ORGANISM: Cryptosporidium parvum
US-09-451-117-2
Search completed: October 2, 2003, 16:36:31 Job time: 36 secs
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US-09-888-655-2
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Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels
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